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Ford, Vanessa
Thursday, October 11, 2001 1:28 PM
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In re: 09596101 Sequence Search

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Inventors (please provide ful	names):				•		
Earliest Priority Filing Da	te:						
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SUMMARIES

Result No.	Score	Query Match Length DB	ength	DB	ID	Description
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N	64	100.0	384	20	AAY24914	Eisenia foetida co
w	50	78.1	306	17	AAR97362	Oerskovia beta-1,3
4	45	70.3	294	22	AAB52463	Mycobacterium tube
ر.	44	68.8	263	18	AAW29455	Oerskovia xanthine
σ	44	68.8	303	18	AAW29457	Oerskovia xanthine
7	44	68.8	435	18	AAW29456	Oerskovia xanthine
8	39	60.9	261	12	AAR11599	Beta-1,3-glucanase
9	39	60.9	292	17	AAR88406	Trichoderma harzia
10	38	59.4	223	21	AAY32318	Corn beta-carotene
11	37	57.8	275	21	AAG44125	Arabidopsis thalia
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ALIGNMENTS

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	Eisenia f	WPI; 1999	De Baetselier P;	(VLAA-) V	17-DEC-1997;	16-DEC-1998;	24-JUN-1999	WO9931229-A2		Eisenia f	inflammat	trypanoso	Eisenia f	Eisenia f	25-AUG-1999	AAY24915;	AAY24915 ID AAY24915	LT 1
Page 45; 49pp; English.	foetida polypeptides derived from coelomic cytolytic factor 1	WPI; 1999-385905/32.	lier P;	(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.	97; 97EP-0203974.	98; 98WO-EP08169.	99.	- 82.		foetida.	inflammation; immunology.	_	foetida; coelomic cytolytic factor 1; CCF-1; cancer;	foetida coelomic cytolytic factor 1 peptide.	99 (first entry)		915 AAY24915 standard; peptide; 13 AA.	

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RESULT
ANY2491
ID AAY2
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Best Local Similarity
Matches 13; Conserv
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The present sequence represents the Eisenia foetida coelomic cytolytic factor 1 (CCF-1). The protein has antiparasitic, antibacterial and antiinflammatory activity. Recombinant coelomic cytolytic factor 1
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                                                                                                    Claim
                                                                                                                                                     Eisenia
                                                                                                                                                                                                                                                                            De Baetselier P;
                                                                                                                                                                                                                                                                                                                             (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eisenia foetida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eisenia foetida; coelomic cytolytic factor 1; CCF-1; cancer; trypanosomal infection; bacterial infection; tumour therapy;
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DB; AAX83611.
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                                                                                                                                                foetida polypeptides derived
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                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-EP08169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= signal
18..384
/label= CCF-1
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1..17
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Pred. No.
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                                                                                                                                                     from coelomic cytolytic factor 1
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A novel

beta-1,3-glucanase (AAR97362) from Oerskovia xanthineolytica

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RESULT
AAR97362
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (rCCF-1) is trypanolytic for the African trypanosome Trypanosoma brucel in a dose-dependent manner. The trypanolytic activity of rCCF-1 can be inhibited by anti-CCF-1 and anti-tumour necrosis factor (TNF)/TIP monoclonal antibodies. Furthermore, N.N'-diacetlychitobiose inhibits potently trypanolytic activity of rCCF-1. These data corroborate the findings that CCF-1 shares a trypanolytic, lectin-like domain with TNF-alpha. CCF-1 is useful to treat trypanosomal or bacterial infections or cancer. The proteins and peptides are also useful in tumour therapy, inflammation and other areas of immunology. The annelid peptide is derived from 42 kDa cytolytic protein named CCF-1 that binds lippolysaccharide and beta-1,3-glucan. The factor resembles the vertebrate tumour necrosis factor-alpha (TNF-alpha), and may be used as an alternative for TNF-alpha.
                                                                                                                                                Savva
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis; lytic enzyme; beta-glucan degradation; cell wall lysis; pigment; colorant; flavour; yeast extract; protoplast.
                                                DNA construct encoding enzyme with beta-1,3-glucanase activity useful for modifying or degrading beta-glucan contg. material a the prepn. of e.g. food colourants, flavourings and yeast extra
                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                             Кеу
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                                                                                                        WPI; 1996-222000/22.
N-PSDB; AAT29043.
                                                                                                                                                                                                                                             16-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        Oerskovia
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                                                                                                                                                                                                                                                                                                                                           Protein
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178 sgeiditetignr 190
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13; Conserv
                        Page 42-43; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     xanthineolytica strain LLG109 (DSM 10297).
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Pred. No.
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ches 0;
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                                                    yeast extracts
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                                                                  and in
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RESULT
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Best Local S
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                                                                                                                                                                                                                   The present invention relates to Mycobacterium tuberculosis secreted proteins (MTSP), where the polypeptide has M. tuberculosis specific antigenic and immunogenic properties. Compositions of the invention may be useful for diagnosing Mycobacterium tuberculosis infection and as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1999;
04-MAY-1999;
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                     Claim 11; Fig 1; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                   polynucleotides useful in tuberculosis -
                                                                                                                                                                                                                                                                                                                                                                             Novel Mycobacterium tuberculosis secreted polypeptides and polynucleotides useful in diagnosis, treatment and prophyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2000
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                                                                                                                                                                                                 vaccine against M.
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80 sgeidimenvgn 191
SGEIDIIETIGN 12
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9; Conserv
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                                                        Similarity 9; Conserv
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                                                          Conservative
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99US-0132503.
                                                                                                                                                                                                   tuberculosis
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75.0%;
                                                                            70.3%;
75.0%;
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                                                                          Score 45;
Pred. No.
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Pred. No. 0.
                                                          Mismatches
                                                                                                                                                                                                   infection
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                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                 22;
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                                                                                                 Length 294;
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Query Match
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Matches 8
                                                                                                                         (see AAT89155). Claimed DNA constructs that encode the hovel of the last of AAW29456 for corrected sequence), a mannose binding domain (see AAW29458) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29456), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                   production of e.g. pigments, colourants, flavourants, extracts, pharmaceuticals, food or feed compositions, prepare protoplasts for use in fusion, transformation
                                                                                                                                                                                                                                                                   This polypeptide comprises a novel Oerskovia xanthineolytica (O: enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amis acid sequence was deduced from an isolated genomic DNA sequence
                                                                                                                                                                                                                                                                                                                                                           New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for
                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW29455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW29455 standard, Protein;
                                                               Sequence
                                                                                         studies.
                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                               for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-526451/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungal cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sgeidliewygn
                                                                                                                                                                                                                                                                                                                       2; Page 35-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVO-NORDISK
                                                                                                                                                                                                                                                                                                                                                                                                    AAT89155
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xanthineolytica mature beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xanthineolytica LLG109
                                                               263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                               AA;
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96DK-0000427
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23..120
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164..952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e; lytic enzyme; yeast; beta glucan degradation;
intracellular product; purification; protoplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
             68.8%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Halkier
                                                                                                                                                                                                                                                                                                                      64pp; English.
Score 44; DB Pred. No. 1.4; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hedegaard L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DSM 10297).
             DB
1.4;
                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                            obtained from Oerskovia
he lysis of microbial cells
                          18;
                         Length 263;
                                                                                                   and cloning
                                                                                                                 and to
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RESULT
AAW29457
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Query Match
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                                                                                                                                                polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the production of e.g. pigments, colourants, flavourants, yeast
                                                                                                                                                                                                                                                        This sequence comprises the polypeptide precursor of a novel oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89157). Claimed DNA constructs that encode the novel BG (see also AAW29455), a mannose binding domain (see AAW29458) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29456), can be used to produce recombinant BG binding domain (see AAW29456), can be used to produce recombinant BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Peptide
                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 42-43;
                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia xanthineolytica, used particularly for the lysis of microbial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-526451/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
fungal cell wall; intracellular product; purification; protoplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oerskovia xanthineolytica beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW29457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW29457 standard; Protein; 303
                                                                                                                      prepare protoplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                 obtaining desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sgeidimenvg 126
 Similarity
8; Conserv
                                                                                                                                      n of e.g. pigments, colourants, flavourants,
pharmaceuticals, food or feed compositions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xanthineolytica LLG109 (DSM 10297).
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                                                                            303
 Conservative
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96DK-0000427.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Sig_peptide 53..303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                      for use in fusion,
              68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                    64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 products
 2,
              Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hedegaard L;
                                                                                                                      transformation and cloning
                              DB 18; Length 303;
 Indels
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RESULT
AAW29456
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PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence comprises the polypeptide precursor of a novel Oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity and which includes a mannose binding domain (MBD). Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89156). Claimed DNA constructs that encode the novel BG lacking a MBD (see AAW29455 and AAW29457), a MDB (see AAW29455), or the full-length enzyme can be used to produce recombinant BC polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key .
                           prepare protoplasts studies.
                                                         productioh of e.g. pigments, colourants, flavourants,
extracts, pharmaceuticals, food or feed compositions,
                                                                                                                                                                                                                                                                                                                   New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia xanthineolytica, used particularly for the lysis of microbial cells for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-526451/48
N-PSDB; AAT89156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation; fungal cell wall; intracellular product; purification; protoplast
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                        Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVO ) NOVO-NORDISK AS
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sgeidimenvg 179
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                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xanthineolytica LLG109 (DSM 10297).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xanthineolytica beta-1,3-glucanase
435 AA;
                                                                                                                                                                                                                                                                                        Page 39-40; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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53..435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                         Halkier T,
                                           use
                                           in fusion,
                                                                                                                                                                                                                                                                                                                                                                                                                         Hedegaard
                                           transformation and cloning
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Query Match Best Local :

Similarity

68.8%;

Score 44; DB Pred. No. 2.5;

18;

Length 435;

RESULT AAR11599

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Matches

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est Local Similarity
atches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          The new enzyme is derived from alkaophhilic Bacillus Sp. The enzyme acts on beta-1,3-glucans to form glucose and laminaribiose. It is stable over a wide pH range with opt. activity at weakly actdic pH and has good heat resistance.
                                               Yeast; fungus; enzyme; endo-beta-glucanase; EC-3.2.1.6; hydrolase; endo-1,3(4)-beta-glucanase; beta-glucan degradation; hydrolysis; detergent; surfactant; fungicide; antifungal; cleaning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat resistant beta-1,3-glucanase gene DNA -alkali-compatible Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-113290/16.
N-PSDB; AAQ11293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-1,3-glucanase
W09531533-A1
                                                                                                    Trichoderma harzianum endo-1,3(4)-beta-glucanase
                                                                                                                              19-AUG-1996
                                                                                                                                                        AAR88406;
                                                                                                                                                                                  AAR88406 standard; Protein; 292 AA.
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Fig 2; llpp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SHKJ ) SHINGIJUTSU KAIHATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alkalophilic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR11599 standard; Protein; 261 AA
                        Trichoderma harzianum CBS
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119 geidimervnn 129
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9 sgeidimenvg 179
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                                                                                                                                                                                                                                                                                                                                                                   261 AA;
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                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heat resistant
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                                                                                                                                                                                                                                                                                                               60.9%;
                        243.71
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                                                                                                                                                                                                                                                                                                                 DB
13;
                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                            Length 261;
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AAY32318
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Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                       Corn beta-carotene hydroxylase.
                                                                                                                                                                                                                                                                                                                                           AAY32318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinantly produced protein are preparation of protoplasts and yeast extracts, brewing, wine and press-juice manufacture, foods and feeds, as antifungal agents, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  raised against a pure endo-1,3(4) beta-glucanase from T. harzianum CBS 243.71. Using this sequence, the protein may be expressed recombinately in transformed host cells, particularly Aspergillus oryzae of Aspergillus niger. Typical applications of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide is immunologically reactive with antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 40; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding endo-beta-glucanase from Trichoderma harzianum useful, e.g., in food processing, as antifungal agent, in cleaning compsns., etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-010920/01.
N-PSDB; AAT09876.
                                                                                                                                                                      04-NOV-1999
                                                                                                                                                                                                WO9955887-A2
                                                                                                                                                                                                                                                  carotenoid;
                                                                                                                                                                                                                                                              Beta-carotene hydroxylase; corn; maize;
                                                                                                                                                                                                                                                                                                                 28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                   AAY32318 standard; Protein; 223 AA.
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Kauppinen MS,
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Novel carotenoid biosynthesis enzyme polynucleotides and polypeptides
                       WPI; 2000-062037/05
N-PSDB; AAZ34967.
                                                                Cahoon RE,
                                                                                                                  24-APR-1998;
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                                                              Kinney AJ,
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                                                                                                                   98US-0083042
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77.8%;
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AAG44125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the deduced amino acid sequence of the C-terminal three quarters of a corn beta-carotene hydroxylase derived from isolated CDNA clones (see AAZ34967). The enzyme converts beta-carotene into Zeaxanthin. The invention provides movel carotenoid biosynthesis C enzymes, specifically beta-carotene hydroxylase, lycopene cyclase C and lycopene epsilon cyclase (see AAZ34967-74). The enzymes may be polynucleotides encoding them (see AAZ34967-74). The enzymes may be create transgenic plants in which the enzymes may be compared recombinantly and used to raise antibodies, used for C prepared recombinantly and used to raise antibodies, used for C detecting the enzymes is situ or in vitro. The polynucleotides may be compared to the enzymes in situ or in vitro. The polynucleotides may be used to create transgenic plants in which the enzymes are c compared to the enzymes or C developmental processes where they are not normally found. This would alter the level of alpha-carotene or beta-carotene in those cells. Zeaxanthin gives a consumer-preferred darker colour to yolks alocking of beta-carotene hydroxylase activity may create a high beta-carotene corn which may be valuable for human consumption. The enzymes can also be used as targets to facilitate the design cand/or identification of inhibitors of those enzymes that may be confided as herbicides. This is desirable because inhibition of any of the enzymes could lead to an inhibition of plant growth.
 25-PEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
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                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
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24 gevpvietlg 33
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99US-0121825.
99US-0123180.
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5; Conservative
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16-APR 1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 EIDIIETIGN 12
|:|:::|||
124 evdvlqvign 133
 6-MAY-1999;
6-MAY-1999;
1-MAY-1999;
1-MAY-1999;
1-MAY-1999;
1-MAY-1999;
1-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thaliana protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000EP-0301439
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990S-0160980

990S-0160989

990S-0161404

990S-0161405

990S-0161406

990S-0161359

990S-0161359

990S-0161920

990S-0161920

990S-0161920

990S-0161920

990S-0161920

990S-0161920
 99US-0121825

99US-012548

99US-0125788

99US-0126785

99US-0127462

99US-0127462

99US-012845

99US-012845

99US-0130077

99US-0130077

99US-013049

99US-0130510

99US-013048

99US-0131449

99US-0132486

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB Pred. No. 39; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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20-MAY-1999
21-MAY-1999
22-MAY-1999
23-MAY-1999
24-MAY-1999
25-MAY-1999
26-MAY-1999
27-MAY-1999
27-MAY
9908-013722

9908-0137502

9908-0137502

9908-0138947

9908-0138947

9908-0139453

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9908-0139457

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990S-0134941.
990S-0135124.
990S-0135353.
990S-0136629.
990S-0136629.
990S-0136392.
990S-0136782.
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RESULT 14
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Best Loc
Matches
                                      is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, anylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate, specificities, catalytic rate, stability, especially in peroxidases. The action of proteolytic enzymes and improved properties such as substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
peroxidase. Note: This sequence is not shown in the specification but is derification the mature B. licheniformis RPII protein [SEQ ID NO: 2] show page 101-102 of the specification (AAE00011). The specification a refers to following variants: (a) VIF, (b) D7G+T125S+E152G+N182I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis Synthetic!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residual proteas mutant; mutein;
                                                                                                                                                                                                                                                                      Norregaard-madsen M,
Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE00115
                                                                                                                                                      The present sequence is Bacillus licheniformis variant (T109R).
                                                                                                                                                                                         Example
                                                                                                                                                                                                             Novel RP-II type protease and its variants useful as constituents detergent compositions, additives and cleaning compositions - \,
                                                                                                                                                                                                                                                                                                        (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                31-AUG-1999;
20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                  31-AUG-2000; 2000WO-DK00476
                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                  2001:226680/23
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5; Conserv
                                                                                                                                                                                        Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease II; RP-II;
mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     licheniformis RP-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 222
                                                                                                                                                                                        Page -; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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990S-0161360.
990S-0161361.
990S-0161920.
990S-0161922.
990S-0161993.
990S-0162142.
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99DK-0001500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 109
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.8%;
                                                                                                                                                                                                                                                                                  Rahbek Ostergaard
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Wild type Thr substituted with Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              additive; cleaning composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease variant (T109R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                 Voge Christensen
                                                                                                                                                                  (BLC) RP-II protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 336;
                          : is derived
2] shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detergent;
              also
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31-AUG-1999
31-AUG-1999

16-AUG-1999 17-AUG-1999

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RESULT 15
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                                                    This invention describes a novel isolated nucleic acid (I) from the genome of phage phi-CH1 of Natrialba magadii. The genome of phi-CH1 is a combination of 48300 and 10198 base pair sequences (S1 and S2), both the fully defined in the specification. The invention also describes a novel (I) recombinant vector (RVI) containing the ori of phi-CH1; (3) cell transformed with RVI or RV2; (4) isolated polypeptide (II) encoded by (I); N. magadii cells free from the prophage of phi-CH1; (5) phage variants having lytic properties different from those of wild-type phi-CH1 and having genomic sequences at least 70 % homologous with the phi-CH1 genome; (6) use of phi-CH1 as gene transfer vector; and (7) use of halophilic Archaea for production of proteins and other polymers. Specifically N. magadii, for production of proteins and other polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (c)
(g)
and
(d),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome; halophilic; polyhydroxybutyrate; inducible expression; 6-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N. magadaii bacteriophage phi-CHl 6-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (c) S119A+S144T+Q157R+S175I, (d) H141A, (e) E152A+Q122R, (f) N182T+C185A, (g) E152A+V144L and (h) E104K+Q204R. However the positions of Val in (a) and (g), Asn residue in (b) and (f), Ser residues in (c), H1s residue in (d), G1n residue in (e) and (h) do not match with the B. licheniformis native wild type RPII protease sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE19937719-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB70788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB70788 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                      Claim 9; Page 41-42; 72pp; German.
                                                                                                                                                                                                                                                                                                                    New nucleic acid from phage phichl, expressing proteins and polymers in
                                                                                                                                                                                                                                                                                                                                                                                                            Witte A, Baranyi U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage phi-CH1.
Natrialba magadii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAF61284.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-245930/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUBI/) LUBITZ W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2001
                            inducible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |:: | ||||
98 gaielsepignr 109
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| |:: | |||
                                          poly(hydroxybutyrate)). Vectors containing
                            expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                Klein
                            compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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Pred. No. 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                     used to create vectors for halophilic Archaea -
                            Archaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω
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                                          (I) allow controlled,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Sequence

419 AA

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Matches 6
3 EIDIIETIGNR 13
                 Similarity 6; Conserv
                  Conservative
                        56.2%;
54.5%;
                       Score 36;
Pred. No.
                  Mismatches
                        DB
81;
                                22;
                                Length 419;
                  Indels
                 0
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Search completed: October 11, 2001, 15:51:38 Job time: 201 sec

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202 didisetlgsr 212

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Result
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Maximum DB
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                         Score
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seq length: 2000000000
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197339 seqs, 20590346 residues
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGEIDIIETIGNR 13
                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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394
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US-07-621-193A-5
US-08-018-488C-5
US-09-08-962-1
US-08-675-507-1
US-09-213-205-1
US-09-213-205-1
US-08-192-632-2
US-08-192-632-2
US-08-192-632-2
US-08-09-992B-2
PCT-US93-06080-2
US-07-867-106-3
US-09-320-878-1
                                                                                                                                                    US-08-712-072C-3
US-08-44
US-08-306-063-44
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US-08-3137-440-44
US-08-329-828C-2
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13.985 Million cell updates/sec
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                                                                                                                               Patent No.
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US-09-189-193-5	US-08-794-524-5	US-08-725-969-5	US-08-504-042-2	US-08-726-817-5	US-08-284-393B-9	US-08-393-305-5	US-08-031-399-2	US-08-300-903A-3	PCT-US94-03793-3	US-09-189-193-6	US-08-794-524-6	US-08-725-969-6	US-08-504-042-3	US-08-726-817-6	US-08-393-305-6	US-08-031-399-3	US-08-343-443B-13
Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 9, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 3, Appli	Sequence 13, Appl

ALIGNMENTS

; TOPOLOGY: 1i ; MOLECULE TYPE: US-08-824-707-2 US-08-824-707-2 Sequence 2, Patent No. APPLICATION NUMBER: US/08/82 FILING DATE: 14-April-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Gregg, Valeta A. REGISTRATION NUMBER: 35,127 REFERENCE/DOCKET NUMBER: 429 GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: APPLICANT: Hedegaard, Lisbeth APPLICANT: Halkier, Torben APPLICANT: Asenjo, Juan APPLICANT: Savva, Demitris TITLE OF INVENTION: No. 5919688el enzyme with beta-1,3-glucanase activity NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 59196880 No. 5919688disk of No. 5919688th America, Inc. STREET; 405 Lexington Avenue, Suite 6400 CITY: New York STATE: New York TELEPHONE: 212-867-0123 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: TYPE: amino acid TOPOLOGY: linear COUNTRY: U.S.A. ZIP: 10174-6401 TELEFAX: 212-878-9655 LENGTH: 306 amino acids Application US/08824707 Diers, Ferrer, Pau protein Ivan US/08/824,707 35,127 4290.204-US #1.25 (EPO)

Query Match Best Local Similarity Conserve

Conservative

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78.1%; 75.0%;

Score 50; DB 2; Pred. No. 0.09; Mismatches

Length 306 Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/OF
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bogosian, Elizabeth A.
RECISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM:PC COM
                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
NUMBER OF SEQUENCES: 13
                                               APPLICANT:
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 TITLE OF INVENTION:
                               APPLICANT:
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146 NGEIDIMEHVG 156
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Kauppinen, Markus Sakari
Christgau, Stephan
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An Enzyme With Endo-1,3(4)-B-Glucanase
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Pred. No.
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Patent No. 6140096
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Best Local
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APPLICATION NUMBER: US/08/737,526
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Valeta, Gregg A
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4174.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acid
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400960 No. 6140096disk of No. 6140096th America, Inc
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                               APPLICANT: Kauppinen, Markus Sakari
APPLICANT: Christgau, Stephan
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APPLICANT: Andersen, Lene No
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                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                       COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                       CITY: New York
STATE: NY
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STRANDEDNESS: si
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                             FILING DATE
                                            APPLICATION NUMBER:
                                                                                                                                                       COUNTRY: USA
ZIP: 10174-6401
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                                                                                                                        Diskette
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77.8%;
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Pred. No. 9.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                       TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION: 212-867-0123
                                                                                                                                                   NAME: CAMPBELL, PAULA A REGISTRATION NUMBER: 32,503 REFERENCE/DOCKET NUMBER: FJJ TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,828C
FILING DATE: 28-TEB-1995
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LENGTH: 292 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                   APPLICATION NUMBER: US/00 FILING DATE: 28-FEB-1995 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                           MOLECULE TYPE:
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                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                               TOPOLOGY:
                                                                           TYPE: amino acid
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NAME/KEY:
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SEKI, NORIAKI
ODA, TOSHIO
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                                                                                           262 amino acids
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Pred. No.
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                                                                                                                                                                                                                                                                                                                    Version #1.25
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                                                                   ; LOCATION: 1..262
; OTHER INFORMATION:
US-09-330-945-37
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Best Local Similarity
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            Query Match
Best Local S
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                                                                                                                                                                                                                         TELEFAX: (617) 248-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617),248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT
NUMBER OF, SEQUENCES: 39
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                             FEATURE:
                                                                                                                                       MOLECULE TYPE:
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                                                                                              NAME/KEY: Protein LOCATION: 1..262
                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: BOSTON
STATE: MA
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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Similarity 7; Conserv.
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                                                                                                                                                                                             262 amino acids
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SEKI, NORIAKI
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 Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                        peptide
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) 248-7100
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            57.8%;
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                                                                                  /note= "BG1 A1 SEQUENCE (FIGURE 2)"
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            Score 37;
Pred. No.
  Mismatches
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19;
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130 SGEIDVMEARG

US-08-712-072C-3

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Query Match
Best Local Similarity
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                                                                                                                            Sequence 44,
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                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 286-0854 or 286-0082 TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                      08-712-072C-3
                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acid
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FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jack Goldstein, Alex Zhu and Lin
TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: PO
HYPOTHETICAL: NO
ANTI-SENSE: NO
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189 SGEIDVMEARG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bogosian, Elizabeth A. REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: NY
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STREET: 9
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                                                                                             INFORMATION:
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                                                                                                                            Application US/08476008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SD
                           Kishore, Ganesh M.
Padgette, Stephen R.
Stallings, William C.
                                                                              Barry, Gerard F.
                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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63.6%;
5-Enolpyruvylshikimate-3-Phosphate Synthases
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Pred. No.
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US-08-306-063-44
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                 Sequence 44,
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                                                                                                                                                           APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 13-SEP-1994
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            265 SGIIDIVEKMG 275
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                     STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hoerner Jr., Denni
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/476,008 FILING DATE: 07-JUN-1995
                                      COUNTRY: USA
ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/749,611 FILING DATE: 28-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                        CITY: St. Louis
                                                                                                         ADDRESSEE: Dennis R. Hoerner, Jr., Monsa
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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700 Chesterfield Village Parkway
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Floppy disk
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63.6%;
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Pred. No.
                                                                                                                           Monsanto Co. BB4F
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,485
FILING DATE: U7-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/749,611
                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                        CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 13-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
APPLICATION NUMBER: US 0 FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SGEIDIIETIG 11.
                                                                                                                                                                                                                                                                                                            DDRESSEE:
                                                                                                                                                                                                                      63198
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                                                                                                                                                                                                                                                          Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08833485
                                                                                                                                                                                                                                                                                         5: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
700 Chesterfield Village Parkway
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                    US 08/306,063
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 430;
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Best Local
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INFORMATION FOR SEQ ID NO:
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TYPE: amino acids
TOPOLOGY: line
(OLECHIE)
           FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/833,485
FILING DATE: 07-APR-1997
                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                        APPLICATION NUMBER: US 0
FILING DATE: 13-SEP-1994
                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
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na. 6248876
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700 Chesterfield Village Parkway
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VENTION: Glyphosate Tolerant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kishore, Ganesh
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                                                                                                                                                                                                                                                                                        Floppy disk
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UMBER: US 07/576,537
31-AUG-1990
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Pred. No.
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Query Match
Best Local Similarity
Watches 7; Conserve
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                                                                                                                                                    TELEFAX: (617) 248-71UU
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
TYPE: amino acid
TYPE: amino acid
                                                Query Match
Best Local Similarity
                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
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                                                                                                                               TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: CAMPELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-033
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: ODA, TOSHIO
ITLE OF INVENTION: NOVEL POTTLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 SGIIDIVEKMG 275
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
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1 SCEIDIIE 8
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SEKI, NORIAKI
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Pred. No.
                                                Score 34; DB 1;
Pred. No. 2e+02;
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                                                               Length 654;
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                                                                                                                                                                                   RESULT
                                                                                                                 GENERAL INFORMATION:
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                 Sequence 2, Application US/09396651B Patent No. 6225076
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                                              APPLICANT: 'Darst, Seth A
APPLICANT: Zhang, Gongyi
APPLICANT: Campbell, Elizabeth
APPLICANT: Minakin, Leonid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atent No.
                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/330,945
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/119,995
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FJ
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                    1 SGEIDIIE 8
T: Severinov, Konstantin
INVENTION: A CRYSTAL OF BACTERIAL CORE RNA POLYMERASE AND METHODS
INVENTION: OF USE THEREOF
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125 HIGH STREET
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SEKI, NORIAKI
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87.5%;
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Pred. No. 2e+02;
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RESULT 15
518080-2
; Patent No. 5180808
; APPLICANT: RUOSLAHTI, ERKKI I.
; TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
; SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
; ANTIBODIES, AND METHODS OF DETECTING THE SAME
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/441,179
; SEQ ID NO:2:
; ELNGTH: 2409
5180808-2
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CURRENT APPLICATION NUMBER: US/09/396,651B
CURRENT FILING DATE: 199-09-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1119
TYPE: PRT
ORGANISM: Thermus aquaticus
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Search completed: October 11, 2001, 15:52:04 Job time: 207 sec
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PROBABLE PROCESSING AND
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InterPro; IPR000501; -.
Pfam; PF01366; PRTP; 1.
Capsid assembly.
SEQUENCE: 782 AA; 87392 MW;
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-99319892;
                                                                                                                                                                                                                                                                                                                                                  Herpesvirus tupaia (Strain 2) (THV-2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=132678;
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36 EQDIVETVGSR 246
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HSSP; P27703; 2;
MGD; MGI:134634
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MITOGEN-ACTIVATED PROTEIN KINASE 7 (EC 2.7.1.-)
REGULATED KINASE 5) (ERK-5) (BMK1 KINASE).
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InterPro; IPR000719; -.
InterPro; IPR002290; -.
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Mammalia; Eutheria;
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"Activation of the protein
kinases: identification and
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MAP KINASE SUBFAMILY.
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PS00107; PROTEIN_KINASE_ATP; 1
PS00108; PROTEIN_KINASE_DOM; 1
PS50011; PROTEIN_KINASE_DOM; 1
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Rodentia;
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kinase ERK5/BMK1 by receptor tyrosine
haracterization of a signaling pathway
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PRO-RICH 1.
POLY-ARG.
PRO-RICH 2.
ATP (BY SIMILAR.
ATP (BY SIMILAR.
BY SIMILARITY.
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Pred. No. 18;
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(BY SIMILARITY).
PHOSPHORYLATION (ACTIVATES THE KINASE)
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          PRT;
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EMBL; U25278; AAA81381.1;
EMBL; U29725; AAA82931.1;
EMBL; U29726; AAA82932.1;
EMBL; U29727; AAA82933.1;
HSSP; P24941; 1AQ1.
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Lee J.-D., Ulevitch R.J., Han J.;

Primary structure of BMK1: a new mammalian map kinase.";

Primary structure of BMK1: a new mammalian map kinase.";

Blochem. Biophys. Res. Commun. 213:715-724(1995).

-1- FUNCTION: MEK5 AND ERK5 INTERACT SPECIFICALLY WITH ONI-
NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHWAYS.

-1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONIN-
PHOSPHORYLATION (BY SIMILARITY).

-1- TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES.

-1- TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES.

-1- TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES.
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DOMAIN 54
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BINDING 83
ACT_SITE 181
MOD_RES 218
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01-NOY-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MITOGEN-ACTIVATED PROTEIN KINASE 7 (EC 2.7.1.-) (
REGULATED KINASE 5) (ERK-5) (ERK4) (BMK1 KINASE).
MAPK7 OR PRKM7 OR ERK5 OR ERK4.
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Lee J.-D., Ulevitch
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MEDLINE-95279403; PubMed-7759517;
Zhou G., Bao Z.O., Dixon J.E.;
"Components of a new human protei
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Mammalia; Eutheria;
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InterPro; IPR002290; -.
Pfam; PF00069; pkinase; 1.
PROSITE; PS01351; MAPK; 1.
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                                                                                                                                                                                                                                                        Serine/threonine-protein kinase;
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PRO-RICH 1.
            ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (ACTIVATES THE KINASE)
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PRO-RICH 2
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SIMILARITY)
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Matches 8
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15-DEC-1998 (
DNA-DIRECTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
SEQUENCE
                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
use by non-profit institutions as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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the Euro
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01-FEB-1996
                                                                                                    Pfam; PF00562; RNA_POL_B; 1.
PROSITE; PS01166; RNA_POL_BETA;
Transferase; Transcription; DNA-
SEQUENCE 1302 AA; 146533 MW;
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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475 GEVDDIDHLGNR 486
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                    2 GEIDIIETIGNR 13
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                                                                                                                                                                                                                                                                                                                                          CATALYTIC
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. 37, Last annotation update)
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. POLYMERASE BETA CHAIN (EC 2.
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Pred. No. 30;
3; Mismatches
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(BY SIMILARITY)
AREGRIRPHRCLCS -> GPVKVEPAHTAASVA (IN
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gene is adjacent to rpoB.";
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RESULT 5
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01-FEB-1995 (Rel. 3
30-MAY-2000 (Rel. 3
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P57146;
01-OCT-2000
                                                                                                                                                   RPOB_BUCAP
P41184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-93160925; Pu Clark M.A., Baumann
                                                          Buchnera aphidicola
Bacteria; Proteobac
                                                                                                      DNA-DIRECTED
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                                                                                                                                                                                                                                                                                                                               Transferase;
SEQUENCE: 1
                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RPOB OR BU034
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01166; RNA_POL_BETA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-TOKYO 1998;
MEDLINE-20445173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       symbiotic bacterium)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-DIRECTED RNA
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*Genome sequence of the endocellular bacterial symbiont of
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                                             NCBI_TaxID=98794;
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440 GEVDDIDHLGNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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BETA' CHAIN.
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. POLYMERASE BETA CHAIN (EC 2.7.7.6)
. POLYMERASE BETA SUBUNIT).
                                                                                         . 31, Last sequence update)
. 39, Last annotation update)
POLYMERASE BETA CHAIN (EC 2.
POLYMERASE BETA SUBUNIT).
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31,
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            PubMed=1369199;
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                                                        c. Schizaphis graminum)
gamma subdivision; Buc
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DNA-directed RNA polymerase.
MW; .95252459873DF940 CRC64;
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Pred. No. 31;
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                                                           Buchnera
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Matches
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PO575; P00576; P78242;
21_JUL_1986 (Rel. 01, Created)
21_NOV-1997 (Rel. 35, Last sequence update)
30_NOV-1997 (Rel. 39, Last annotation update)
DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE RETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
RETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
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Nucleic
[3]
                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-61260785; PubMed-6266829;

MCChertov O.Y., Modyanov N.N., Grinkevich V.A., M.

Marchenko T.V., Polovnikova I.N., Lipkin V.M., Grinkevich V.A., M.

Marchenko T.V., Polovnikova I.N., Lipkin V.M., Grinkevichia coli RNA
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PROSITE; PS01166; RNA_POL_BETA; 1.
Transferase; Transcription; DNA-directed RNA polymerase.
SEQUENCE 1342 AA; 152060 MW; 7E30BC9E013D31ED CRC64;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
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-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCI OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
                   Daniels D.L.;
"Analysis of the Escherichia coli
region from 89.2 to 92.8 minutes "
Nucleic Acids Res. 21:5408-5417(19
                                                                                                                                                                                     "The primary structure of sequence of the rpoB gene beta-subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of an aphid endosymbiont DNA fragment containing rpoB (beta-subunit of RNA polymerase) and portions of rplL and rpoC
                                                                                    Blattner F.R.,
                                                                                                      STRAIN-K12 / MG1655;
MEDLINE-94089392; Pu
                                                                                                                                       SEQUENCE FROM
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cland V.D., Plunkett
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SEQUENCE OF 187-33-.
Sverdlov E.D., Lipkin V.M., ru...
Guryev S.O., Chertov O.Y.;
"The nucleotide sequence of strong RN the E.coli rpoB structural gene.";
the E.coli sequence of strong RN thim. 6:309-312(1980).
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Ovchinnikov Y.A., Sverdlov E.D., Lipkin V.M., Monastyrskaya G.
Chertov O.Y., Gubanov V.V., Guryev S.O., Modyanov N.N.,
Grinkevich V.A., Makarova I.A., Marchenko T.V., Polovnikova I.
"Primary structure of RNA polymerase from E. coli; nucleotide
of EcoRl-C fragment of gene rpoB and amino acid sequence of the corresponding fragment of beta-subunit.";
Bioorg. Khim. 6:655-665(1980).
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Miller E.
                                                                                                                                                                                                                                                                                                                       Gurevich A.I., Igoshin A.V., Kolosov M. "Structure of a central part of E.coli sequence of the gene for beta subunit o
                                                             MUTAGENESIS OF GLU-813.
MEDLINE=91296752; PubMed=2068078;
Lee J., Kashlev M., Borukhov S.,
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"RNA polymerase beta-subunit.
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the beta-subunit.";
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D., Lipkin V.M., Monastyrskaya G.
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                                                        SEQUENCE FROM N.A. SURVEY S.O., Monastyrskaya G.S.; SverdLov E.D., Lisitsyn N.A., Guryev S.O., Monastyrskaya G.S.; "Nucleotide sequence of the rpoB gene of Samonella typhimurium for the beta-subunit of RNA polymerase."; Dokl. Biochem. 287:62-65(1986).
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58.3%;
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E->K: DISRUPT THE ENZYME'S A(
ER -> G (IN REF. 5).
LFENLFFS -> CSRTCSSPT (IN REI
D -> V (IN REF. 1 AND 9).
11 MW; F9E95344C54AB118 CRC64;
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                                                                                                                                                                                                                        subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                           1342 AA
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MBL outstation -
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P43738;
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"Genes coding for RNA polymerase beta
Structure/function analysis.";
Eur. J. Biochem. 177:363-369(1988).
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00562; RNA_POL_B; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
Transferase; Transcription; DNA-directed RNA polymerase.
CONFLICT 401 401 G -> A (IN REF. 3).
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EMBL; M38311; AAA27215.1;
PIR; S01794; RNEBBT.
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Bioorg. Khim. 12:699-707(1986).
-i-FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sverdlov E.D., Lisitsyn N.A., Guryev Rostapshov V.M., Monastyrskaya G.S., "Genes encoding the beta-subunit of b Primary structure of the EcoRI-C frag
                                                                                                                                                                                                                                                                 DNA-DIRECTED
BETA CHAIN) (
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                    Fleischmann R.D., Adams M.
Kerlavage A.R., Bult C.J.,
                                                         STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
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                                                                                                              SEQUENCE
                                                                                                                                                     NCBI_TaxID=727;
                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                   Haemophilus
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                                                                                                              FROM
                                                                                                                                                                                               Proteobacteria;
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                                                                                                                                                                                                                                                               (Rel. 32, Created)
(Rel. 32, Last sequence update)
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D RNA POLYMERASE BETA CHAIN (EC 2.7)
(RNA POLYMERASE BETA SUBUNIT).
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150557 MW;
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                  M.D., White
J., Tomb J.-I
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Pred. No.
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Mismatches
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EDBF979D3E9E4DE8 CRC64;
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Dougherty B ields C.A., (
                    Clayton R.A., Kirkness E.
Dougherty B.A., Merrick J.
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InterPro; IPRO01572; -.
Pfam; PF00562; RNA_POL_B; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
Transferase; Transcription; DNA-directed RNA
Transferase; Tanscription; DNA-directed RNA
Transferase; Transcription; DNA-directed RNA
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the Euro
                                         STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-2022556; PubMed-10761919;
Parkhill J. Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Bavies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jayels K., Leather S., Moule S., Mungall K., Quall M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
menigitidis 22491."
"menigitidis 22491."
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-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
-I- FUNCTION: DNA-GETMG THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
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01-OCT-2000
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Venter J.C.;
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Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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Weidman J.F., Phillips C.
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Bacteria; Proteobacteria; beta sub
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                            Nature 404:502-506(2000).
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FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
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                                                                                                                                                                                                                                                                                       (RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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POLYMERASE BETA CHAIN (EC 2.7,
POLYMERASE BETA SUBUNIT).
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                                                                                                                                                                                                                                           erogroup A).
beta subdivision;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
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RESULT 11
RPOB_NEIMB
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Best Local :
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                                                                                                                                                            Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Dougherty B.A., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Kouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPOB_NEIMB
Q59622;
                                                                                      MC58.";
Science 287:1809-1815(2000).
-i- function: DNA-DEPENDENT RNA POLYMERASE CATALY?
-i- function: DNA-DEPENDENT RNA POLYMERASE CATALY?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (see http://www.isb-slb.or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-DIRECTED
BETA CHAIN) (
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sul
                                                                                                                                                                                                                                                                                                                                                                                                                                       RPOB OR NMB0132
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01-OCT-2000
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                                          <del>:</del>
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01166; RNA_POL_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=491;
                                                                                                                                                   'Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 GEVDDIDHLGNR 478
RNA(N).
- SUBUNIT: THE ENZYME WHICH BETA' CHAIN.
- SIMILARITY: B
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CATALYTIC A
RNA(N).
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SIMILARITY:
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                                                                    CATALYTIC
                                                                                SUBSTRATES
                                                                                                                                                                                                                                                                                                                                             0.J.;
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                                                                                                                                                                                                                                                                                                                               (OCT-1995)
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
D RNA POLYMERASE BETA CHAIN (EC 2.7.7.
(RNA POLYMERASE BETA SUBUNIT).
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                                                                     ACTIVITY: N
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  BELONGS
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                          SI
                                          ENZYME
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58.3%;
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                                                                     NUCLEOSIDE TRIPHOSPHATE -
                                                                                                                                                                                                                                                                                                                                                                                                               beta subdivision; Neisseriaceae; Neisseria
  THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-directed RNA polymerase. MW; BA4AF438619CB82C CRC64;
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ALPHA
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32;
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LEOSIDE TRIPHOSPHATES
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  BETA
                                          CHAIN
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9
                            IN AND THE C
BETA CHAIN,
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                                                                     N PYROPHOSPHATE
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RESULT 12
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Best Local
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01-OCT-1996
01-OCT-1996
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                                                                                                                     SEQUENCE FROM N.A.
Zabel U., Doye V., Te
Submitted (JAN-1996)
                                                                                                                                                                                                                                                                     P52593;
                                                                                                                                                                                                                                                                              N188_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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PROSITE; PS01166; RNA_POL_BETA;
                  STRAIN-S288C / AB972;
Devlin K., Churcher C.,
Submitted (AUG-1994) to
                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                             NUP188 OR YML103C
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                                                     SEQUENCE FROM N.A
                                                                                    SEQUENCE FROM N.A.
Nehrbass U., Rout
                                                                                                                                                                 NCBI_TaxID-4932;
                                                                                                                                                                              Saccharomycetales;
                                                                                                                                                                                                                        NUCLEOPORIN NUP188 (NUCLEAR PORE PROTEIN NUP188).
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SEQUENCE OF 1187-1205 AND 1611-1629
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AE002371; AAF40591.1; ALT_INIT.
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                                                                          U., Rout M.P., (FEB-1996) to
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350
378
648
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818
837
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    Last sequence update)
    Last annotation update)

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378
378
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58.3%;
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                  Barrell B.G.,
the EMBL/GenB
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                                                                                    Maguire S.,
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GG -> A (IN REF. 1).

F -> L (IN REF. 1).

GY -> VN (IN REF. 1).

YNG -> SR (IN REF. 1).

A -> S (IN REF. 1).

DDP -> EDA (IN REF. 1).

F -> L (IN REF. 1).

WW; 92AA331A597898F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-directed RNA polymerase
N -> S (IN REF. 1).
L -> I (IN REF. 1).
                                                                                                                      H., Wepf R., Hurt E.C.; EMBL/GenBank/DDBJ databases
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                    EMBL/GenBank/DDBJ
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Pred. No.
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A -> G (IN REF. 1).
A -> P (IN REF. 1).
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RNVLFVFKRCSNRFGRRPSES (IN REF.
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                                                                                      Blobel G.,
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                                Rajandream M.A.;
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32;
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                      databases
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                                                                                      Wozniak R.W.;
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
BETA-GLUCAMASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCAMASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                  This
                                                                                                -I: FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAM
BUT NOT ON CMC CELLULOSE OR XYLAN. THE ENZYME HAS A TEMPE
OPTIMUM OF 85 DEGREES CELSIUS AND A PH OPTIMUM OF 7.0.
-I: CATALYTIC ACTIVITY: HYDROLYSIS OF 1.4-BETA-D-GLYCOSIDIC
LINKAGES IN BETA-D-GLUCANS CONTAINING 1.3- AND 1.4-BONDS.
-I: SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein; Transcouence 1655 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X90580; CAA62208.1; -. EMBL; U47107; AAA88904.1; -. EMBL; X80835; CAA56794.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                        Spilliaert R., Hreggvidsson G.O., Kristjansson J.K., Eggertsson G. Palsdottir A.; "Cloning and sequencing of a Rhodothermus marinus ge for a thermostable beta-glucanase and its expression
                   use
                               between the Swiss Institute of Bioinfi
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                      MEDLINE-95010084; PubMed-7925416;
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                              Rhodothermus marinus
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SUBUNIT: INTERACTS WITH NUP170 AND/OR POM152.
                                                 SWISS-PROT entry is copyright. It is produced through a collaboration -
een the Swiss Institute of Bioinformatics and the EMBL outstation -
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8; Conserv
non-profit institutions and this statement is not
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AA; 188576 MW;
                                                                                                                                                                                                                                                                                                                                                                                            Rhodothermus group; Rhodothermus
                   institutions as long
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                 There are no restrictions ng as its content is in
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A TEMPERATURE
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01-FEB-1996
15-DEC-1998
15-DEC-1998
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Hydrolase;
SIGNAL
CHAIN
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                         CANAL
                                                                                                                                                                the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIR-ATCC 10231;
MEDLINE-96367593; PubMed-8771707;
MEDLINE-96367593; PubMed-8771707;

Stoldt V., Rademacher F., Kehren V., Ernst J.F., Sherman F.;

"Review: the Cct eukaryotic chaperonin subunits of Saccharomyces cerevisiae and other yeasts.";

Yeast 12:523-529(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida albicans (Yeast).
Eukaryota: Fungi; Ascomycota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U04836;
HSSP; P23904;
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                       InterPro; IPR002194; InterPro; IPR002423;
                                                                                 EMBL; U37371; AAC31764.1;
                                                                                                                                              entities requires
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                                                                                                                        s requires a license agreement (S an email to license@isb-sib.ch).
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PS01034; GLYCOSYL_HYDROL_F16;
PS00750; TCP1_1;
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98 (Rel. 37, Last sequence update)
98 (Rel. 37, Last annotation update)
PROTEIN 1, THETA SUBUNIT (TCP-1-T
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PROTON DONOR (BY SIMILARITY);
7215C33624135191 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ion update)
(TCP-1-THETA) (CCT-THETA).
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RESULT 15
CNG_DROME
Pfam; PF00914; CNG_membrane; 1.

Pfam; PF00917; CNMP_BINDING_1; 1.

R Pfam; PF00927; CNMP_BINDING_1; 1.

R PROSITE; PS00888; CNMP_BINDING_2; 1.

PROSITE; PS00889; CNMP_BINDING_2; 1.

PROSITE; PS50042; CNMP_BINDING_3; 1.

PROSITE; PS50042; CNMP_BINDING_2; 1.

PROSITE; PS50042; CNMP_BINDING_2; 1.

PROSITE; PS50042; CNMP_BINDING_2; 1.

PROSITE; PS00889; CNMP_BINDING_2; 1.

PROSITE; PS00089; CNMP_BINDING_2; 1.

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Q24278;
Q1-NOV-1997
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MEDLINE-95045396; PubMed-7957070;

Baumann A., Frings S., Godde M., Seifert R., Kaupp U.B.;

Baumann A., Frings S., Godde M., Seifert R., Kaupp U.B.;

Primary structure and functional expression of a Drosophila cyclic nucleotide-gated channel present in eyes and antennae.";

EMBO J. 13:5040-5050(1994).

-I- FUNCTION: APPROXIMATELY 50-FOLD MORE SENSITIVE TO CGMP THAN TO CAMP. MAY BE INVOLVED IN TRANSDUCTION CASCADES OF BOTH INVERTEBRATE PHOTORECEPTORS AND OLFACTORY SENSILLAE.

-I- TISSUE SPECIFICITY: EXPRESSED IN ANTENNAE AND THE VISUAL SYSTEM.

-I- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00751; TCP1_2; 1.

PROSITE; PS00995; TCP1_3; FALSE_NEG.
Chaperone; ATP-binding; Multigene family.
SEQUENCE 540 AA; 58918 MW; F962285DA6EB03DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a copyright the EMBL between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (CNG CHANNEL).
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR000595;
InterPro; IPR002025;
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Pred. No.
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Copyright (c) 1993 - 2000 Compugen
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01-NOV-1998 (Tremblrel. 08, La
01-NOV-1998 (Tremblrel. 08, La
COELOMIC CYTOLYTIC FACTOR 1.
Q51333;
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MEDLINE=98406152; PubMed=9733802;

Beschin A., Bilej M., Hanssens F., Raymakers J., Van Dyck E.,

Beschin A., Bilej M., Hanssens F., Raymakers J., Van Dyck E.,

Revets H., Brys L., Gomez J., De Baetselier P., Timmermans M.;

"Identification and cloning of a glucan- and lipopolysaccharide-
binding protein from Eisenia foetida earthworm involved in the
activation of prophenoloxidase cascade.";

J. Biol. Chem. 273:24948-24954(1998).

EMBL; AF030028; AAC35887.1;

SEQUENCE 384 AA; 44322 MW; C90BSC94003BAD6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eisenia foetida (Common brandling worm) (Common dung-worm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Hapl
Lumbricina; Lumbricidae; Eisenia.
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tive 0; Mismatches 0.
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SIGNAL
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                                                                                                                                                                                                                                                                              Lee S., Wang R., Soderhall K.;

**A lipopolysaccharide- and beta-1,3-glucan-binding hemocytes of the freshwater crayfish Pacifastacus l purification, characterization, and cDNA cloning.;

J. Biol. Chem. 275:1337-1343(2000).
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-HEMOCYTES;
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Eumalacostraca; Euca
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HSSP; P23904;
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MEDLINE=96345651; PubMed-8755914;
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                                   SGEIDIIETIGN 12
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 SGEIDIVESRGN 183
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9; Conserv
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9; Conser
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AAC44371.1; -.
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Eucarida; Decapo
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BETA-1,3-GLUCAN BINDING PROT
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Decapoda; Pleocyemata; Astacic
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Pred. No.
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Mismatches
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01-JUL-1997 (TrE
01-JUL-1997 (TrE
01-JUN-2000 (TrE
PROBABLE BETA-1,
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COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H
GOrdon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekkaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hol-
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Suls
Taylor K., Whitehead S., Barrell B.G.;
Taylor K., Whitehead S., Barrell B.G.;
Teciphering the biology of Mycobacterium tuberculosis from to complete genome sequence.";
Native 203.637564/10080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q26660;
Q26660;
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Nature 393:537-544(1998).
EMBL, Z96800; CAB09586.1;
TubercuList; Rv0315;
TuterPro; IPR000757;
SR01034; GLYCOSYL_HYDROL_F16; UNKNOWN_1
SEQUENCE 294 AA; 32186 MW; 7B9897BA6740BEB0
                                                                                                          "Molecular cloning of the first metazoan beta-1,3 of the sea urchin Strongylocentrotus purpuratus."; Proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996). EMBL; U49711; AAC47235.1; SEQUENCE 499 AA; 55274 MW; D863F36EEOCFF5AC CR
                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotus purpuratus (Purple Eukaryota; Metazoa; Echinodermata; Ele
Echinoidea; Euechinoidea; Echinacea; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                  Strongylocentrotus.
NCBI_TaxID=7668;
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Score 45; DB
Pred. No. 9.5;
3; Mismatches
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Pred. No. 5.1;
1; Mismatches
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a; Echinoida; Strongylocentrotidae;
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Bacteria; Firmicutes; Actinobacteria; Actinobacter1uae;
Bacteria; Firmicutes; Actinobacteria; Actinobacter1uae;
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01-MAR-2001 (TrEMBLrel.
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01-AUG-1998
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"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
EMBL; AL445945; CAC14352.1; -.
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Cerdeno A.M.,
                                                                                                                                                              Enzyme Microb.
                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-LL G109;
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NCBI_TaxID=1902;
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Q9F3A0;
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                                                                                                                                    Redenbach M., Kieser H.M.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids a
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Ferrer P., Hedegaard L., Halkler T., Diers I.
"Molecular cloning of a lytic beta-1,3-glucan
xanthineolytica LLG109. A beta-1,3-glucanase
permeabilize the yeast cell wall.";
Ann. N. Y. Acad. Sci. 782:555-566(1996).
                                                   the 8 Mb Streptomyces coelicolor Mol. Microbiol. 21:77-96(1996). EMBL; AL450165; CAC16455.1; -.
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"Molecular characterisation of a thermoactive beta-1,3-glucanase Oerskovia xanthineolytica.";
SEQUENCE
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Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
SMART; SM00458; RICIN; 1.
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6977A032A1A31451 CRC64;
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,3-glucanase gene
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Best Local Similarity
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Best Local S
Matches 7
                                                                                                                                                                                                                                      Q9KJG4;
01-OCT-2000
01-OCT-2000
01-MAR-2001
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01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                  Q9KJG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00562; RNA_pol_B; 1.

PROSITE; PS01166; RNA_POL_BETA; 1.

DNA-directed RNA polymerase; Transcription; Transferase.

SEQUENCE 1383 AA; 154780 MW; 9B007A67C872498E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bartonella quintana (Rochalimaea quintana).
Bacteria; Proteobacteria; alpha subdivision
Bartonellaceae; Bartonella.
Renesto P., Gouvernet J., Dra "New approach to identifying rpoB gene sequencing.";
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                                                             SEQUENCE FROM N.A. STRAIN-HOUSTON-1;
                                                                                                                   Bartonellaceae; B
NCBI_TaxID=38323;
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                                                                                                                                                         Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; alpha subdivision;
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Matches 8
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Best Local
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InterPro; IPR002049;
PRINTS; PR00011; EGFLAWNIN.
PROSITE; PS00022; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; 2.
EGF-11ke domain; Glycoprotein; Hypoth SEQUENCE 736 AA; 84202 MW; 349E0F
  Q9F406;
Q9F406;
01-MAR-2001
01-MAR-2001
01-MAR-2001
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-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
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Pfam; PF00562; RNA_POL_B; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
DNA-directed RNA polymerase; Transcription; Transferase.
SEQUENCE 1383 AA; 154852 MW; 2CEE87E06A3207B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benes V., Rechmann S., Mayer K.F.X., Lemcke K Submitted (APR-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA(N) (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO EMBL; AF171070; AAF87049.1;
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Submitted (JUN-1999) to the
EMBL; AL049660; CAB41192.1;
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8; Conservative
  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                         PRELIMINARY;
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Created)
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Pred. No.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-B:4:P1.10;
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Neisseria meningitidis.
Bacteria; Proteobacteria;
NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                 "Rifampin-resistant meningococci causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mastrantonio P.;
                                                                                                                                                                                                                                                                                                           the strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rifampin-resistant meningococci causing invasive
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 36
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GEVDDIDHLGNR
                                     GEIDIIETIGNR
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AJ270500; CAC14804.1;
AJ270503; CAC14807.1;
                                                                          Similarity 58.: 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 58.: 7; Conservative
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342 AA;
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342 AA;
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L (TrEMBLIE1. 16, 1
L (TrEMBLIE1. 16, 1
RASE BETA SUBUNIT
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; 37264 MW;
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37253 MW;
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58.3%;
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58.3%;
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Pred. No.
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Pred.
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3a G., 1
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                                                                                                                                                                         2CD9BD9709A5DEDE CRC64;
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Marianelli C.,
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48;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
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1: /SIDS8/acad>+:
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/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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2240
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	•			SUMMARIES	
	Query				•
Score	Match	Length	•	Ħ	Description
2240	100.0	384	20	AAY24914	Eisenia foetida co
350	15.6	303	18	AAW29457	Oerskovia xanthine
350	15.6	435	18	AAW29456	Oerskovia xanthine
340.5	15.2	263	18	AAW29455	Oerskovia xanthine
314	14.0	455	17	AAR89136	Bombyx mori mature
314	14.0	467	17	AAR89137	Bombyx mori full l
310	13.8	261	12	AAR11599	Beta-1,3-glucanase
296	13.2	306	17	AAR97362	Oerskovia beta-1,3
286.5	12.8	422	19	AAW56275	Flavobacterium ker
209	9.3	673	16	AAR67915	(1-3)-beta-D-gluca
208	9.3	233	16	AAR67918	(1-3)-beta-D-gluca
	· 1	· 1	· 1	Query Hength DB Match Length DB 100.0 384 20 15.6 303 18 15.2 263 18 15.2 263 18 15.4 455 17 14.0 455 17 13.8 261 12 13.2 306 17 12.8 422 19 9.3 673 16	Query

Arabidopsis thalia	AAG36454	21	296	4.3	96	45
S	AAG43412	21	286		96	44
ŝ	AAG36455	21	286		96	43
Arabidopsis	AAG43413	21	281		96	42
Ar	AAG36456	21	281		96	41
В.	AAW93001	20	308	4.4	98.5	40
Ну	AAR06621	11	239	•	98.5	39
An	AAY54011	21	539		99	38
Ну	AAR06622	11	237	•	100	37
. Ar	AAG48467	21	282		100.5	36
	AAG11993	21	291	4.5	101.5	35
Ar	AAG11994	21	281		101.5	34
Ar	AAG11995	21	274		101.5	ω u
Arabidopsis	AAG52470	21	291		102.5	32
S	AAG52471	21	281		102.5	31
	AAG52472	21	274	4.6	102.5	30
idopsis	AAG40081	21	. 316		103	29
5	AAG40082	21	289	٠	103	28
	AAG07535	21	317	٠	105	27
is thali	AAG07536	21	289	4.7	105	26
Gene 21 human secr	AAB63197	21	280		107	25
Cytophaga drobachi	AAW50908	19	545	٠	107.5	24
Arabidopsis thalia	AAG32464	21	282	٠	108	23
Arabidopsis thalia	AAG18642	21	298	٠	111	22
Arabidopsis thalia	AAG18643	21	282		111	21
Arabidopsis thalia	AAG18644	21	269		111	20
. A.altocetigenes me	AAR13993	12	738	٠	111.5	19
Ruminococcus flave	AAB48550	21	954		12.	18
ADH complex protei	음	13	738		12.	17
Bankia gouldi endo	AAW34987	19	875	٠	13.	16
Phaffia rhodozyma	AAW77311	19	424		21.	15
rzi	84	17	292		31.	14
ycobacterium	AAB52463	22	294	6.2	138.5	13
Streptomyces sp. 9	231	20	341		68.	12

ALIGNMENTS

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RESULT AAY24914
AAY24914 standard; Protein; 384 AA.
         De Baetselier P;
                                                17-DEC-1997;
                                                                                         24-JUN-1999.
                                                                                                              WO9931229-A2.
                                                                                                                                                                                             Eisenia foetida.
                                                                                                                                                                                                                trypanosomal infection; b inflammation; immunology.
                                                                                                                                                                                                                        Eisenia foetida; coelomic cytolytic factor 1; CCF-1; cancer; trypanosomal infection; bacterial infection; tumour therapy;
                                                                                                                                                                                                                                                      Eisenia foetida coelomic cytolytic factor 1 protein.
                                                                                                                                                                                                                                                                           25-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                AAY24914;
                            (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                    16-DEC-1998;
                                                                                                                                           Protein
                                                                                                                                                              Peptide
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__
                                                 97EP-0203974.
                                                                    98WO-EP08169.
                                                                                                                                /label= signal
18..384
/label= CCF-1
                                                                                                                                                                 Location/Qualifiers
1..17
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WPI; 1999-385905/32

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CC factor 1 (CCF-1). The protein has antiparasitic, antibacterial and CC antinflammatory activity. Recombinant coelomic cytolytic factor 1 (CCF-1) is trypanolytic for the African trypanosome Trypanosoma brucei CC in a dose-dependent manner. The trypanolytic activity of rCCF-1 can be CC inhibited by anti-CCF-1 and anti-tumour necrosis factor (TMF)/TIP CC monoclonal antibodies. Furthermore, N,N'-diacetlychitobiose inhibits CCF indings that CCF-1 shares a trypanolytic, lectin-like domain with CCF indings that CCF-1 is useful to treat trypanosomal or bacterial infections CC or cancer. The proteins and peptides are also useful in tumour therapy, CC derived from a.42 kDa cytolytic protein named CCF-1 that binds cc derived from a.42 kDa cytolytic protein named CCF-1 that binds cc derived from a.42 kDa cytolytic protein named CCF-1 that binds cr useful and beta-1,3-glucan. The factor resembles the vertebrate tumour necrosis factor-alpha (TMF-alpha), and may be used as an alternative for TMF-alpha.
                                                                                                                                                                                                                                                                                                                             24
AAW29457
ID AAW2
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AC AAW2
DT 14-P
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DE Oers
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KW Betz
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Best Local
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                                                             Oerskovia xanthineolytica beta-1,3-glucanase
                                                                                                                                                         AAW29457 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
              Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation; fungal cell wall; intracellular product; purification; protoplast
                                                                                            14-APR-1998
                                                                                                                           AAW29457
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                                                                                                                                                                                                                                     KWTWDDEGDNNAMQVDYIRVYKRN 384
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                                                                                                                                                                                                                                                                                                                                     LAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW 360
                                                                                                                                                                                                                                                                                                                                                                   FWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gaagdippamsarvrtfqkysfthgrvvvhakmpvgdwlwpaiwmlpedwvyggwprsge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gansfvrdgklfikptlladninpqtgapfgtdfmyngvldvwamygactntdnngcyrt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 AA;
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2240; DB 20;
Pred. No. 1.2e-204;
); Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence comprises the polypeptide precursor of a novel cerskovia xanthineolytica enzyme that exhibits beta-1.3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAW29457). Claimed DNA constructs that encode the novel BG (see also AAW29455), a mannose binding domain (see AAW29458) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29456), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         prepare protoplasts studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                       production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated beta-1,3-glucanase enzyme - ol
xanthineolytica, used particularly for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-526451/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 42-43; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS
                                 188
                                                               201
                                                                                              132
                                                                                                                              141
                                                                                                                                                               106
 261 LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN 320
                                                                                                                                                                                             81
                                                                                                                                                                                                                             57
                                                                                                                              SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
                                                                                                                                                                                                                                          IVWQDEFDYFDG----AKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLAD
                               -----tvh-gpgysggs-gitgmyqhpqgwsfadtfhtfavdwkpgeitwfvd--gqq
                                                               GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA
                                                                                             qpqygrieariqiprgqgiwpafwmlggsfpgtpwpssgeidimenvgfephrvhg----
                                                                                                                                                                                               NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                          llwsdefdgaagsapnpavwnhetgahgwgnaelqnytasransal-dgq-----
                                                                                                                                                                                                                                                                                           103;
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                                                                                                                                                                                                                                                                                                                                                                           303
                                                                                                                                                                                                                                                                                           Conservative
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96DK-0000427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                        cicals, food or feed compositions, and to for use in fusion, transformation and cloning
                                                                                                                                                                                                                                                                                                          15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halkier T,
                                                                                                                                                            -gnlvita----rregdgsy-----tsarmttqgky 131
                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                         Score 350; DB 18;
Pred. No. 3.1e-25;
30; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hedegaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            obtained from Oerskovia
he lysis of microbial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
                                                                                                                                                                                                                                                                                                                         Length 303;
                                                                                                                                                                                                                                                                                            Indels 132;
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                              80
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RESULT AAW29456

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BXAXB

AAW29456;

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This sequence comprises the polypeptide precursor of a novel oberskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity and which includes a mannose binding domain (MBD). Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89156). Claimed DNA constructs that encode the novel BG lacking a MBD (see AAW29455 and AAW39457), a MBD (see AAW29455), or the fill-length enzyme can be used to produce recombina BG polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for obtaining desirable products
                                              production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1996;
12-APR-1996;
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fungal cell wall; intracellular product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oerskovia xanthineolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 39-40; 64pp; English.
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DB; AAT89156.
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                        protoplasts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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96DK-0000427.
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    obtained from Oerskovia
the lysis of microbial cells

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purification; protoplast.
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Best Local
                   Diers I,
                                                                                                                            23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-1,3-glucanase;
fungal cell wall; in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oerskovia xanthineolytica mature beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW29455 standard; Protein;
                                                                       (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                              23-OCT-1997.
                                                                                                                                                                                                                                                                                                               WO9739114-A1
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                                                                                                                                                                                                         14-APR-1997;
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96DK-0000427
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23..120
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164..952
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                   Halkier
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Pred. No. 4.9e-25;
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                   Hedegaard
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Domain Protein Peptide

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89155). Claimed DNA constructs that encode the novel BG also AAW29456 for corrected sequence), a mannose binding domain (AAW29458) or a full-length enzyme, i.e. BG with mannose binding
           Bombyx mori mature LPS-binding protein
                                           22-AUG-1996
                                                                          AAR89136
                                                                                                       AAR89136 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises a novel Oerskovia xanthineolytica (OX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia xanthineolytica, used particularly for the lysis of microbial cells for obtaining desirable products
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N-PSDB; AAT89155.
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                                                                                                                                                                                                                                                                             GFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRV
                                                                                                                                                                                                                                                                                                                                 LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            llwsdefdgaagsapnpavwnhetgahgwgnaelqnytasransal-dgg------
                                                                                                                                                                                                                                                                                                                                                                                                     GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFYDDENQA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                  qpqygrieariqiprgqgiwpafwmlggsfpgtpwp-sgeidimenvgfephrvhg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                          (first entry)
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                                                                                                       protein; 455 AA.
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28.5%;
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Pred. No. 2e
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2e-24;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding protein from Bombyx mori. The protein was isolated haemolymph of fifth stage B.mori larvae after injection with Enterobacter cloacae strain 57-9. Partial amino acid sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 41-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipopoly-saccharide - esp. used to treat septic shock, also encoding it, for producing transgenic plant(s) resistant to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lipopolysaccharide binding protein; Bombyx mori; haemolymph; primer; Enterobacter cloacae; PCR; polymerase chain reaction; amplification; probe; LPS complex; septic shock; injection; transgenic plant; vine; tobacco; tomato; potato; fungal infection; fungus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of a mature lipopolysaccharide (LPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protein from Bombyx mori that binds bacterial lipopoly-saccharide - esp. used to treat septic :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-060094/07
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Modified-site
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 315
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                                                                                                                                                                                                                                                                                                                                           27 VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ 85
AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN 370
                                                                   DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                                                                                      GGEFLGIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
                                                                                                                                                                                                        HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN-----RDFKNT 195
                                                                                                                                                                                                                                       qhmpgflddsiysgtln---lfsgctss-aeaclkqasgadilppivsgri-tsigfaft
                                                                                                                                                                                                                                                                         TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT 143
                                                                                                                                                                                                                                                                                                         ifeeqfdsldenvwqieqyipiyhpeypfvsyqrnnltvstadgnlhi----naklq 187
                                                                                                   -----vlyggpimdlecrenflstkrrrdgtswgdsfhtysvgwtpdfialsv
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                                                                                                                                                                                                                                                                                                                                                                                            Score 314; DB 17;
Pred. No. 1.4e-21;
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                               pavcahaprhllqagsqmapfddhfy1tlgv
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fungal
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RESULT
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              Query Match
Best Local !
Matches
                                                                                       This is the amino acid sequence of the full length lipopolysaccharide (LPS) binding protein from Bombyx mori. The protein was isolated from the haemolymph of fifth stage B.mori larvae after injection with Enterobacter cloacae strain 57-9. Partial amino acid sequence was used to generate PCR primers (AAT10280-1). These amplified a fragment of the gene used as a probe to obtain the full length gene by screening a cDNA library derived from B.mori previously injected with heat-killed scloacae. The protein or fragments of it, can be used to treat diseases associated with LPS complexes e.g. septic shock, to remove LPS from products used for injection and to protect transgenic plants e.g. vines, tobacco, tomato or potato, against fungal infections.
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                                                                                                                                                                                                                                                                                                     New protein from Bombyx mori that binds bacterial lipopoly-saccharide - esp. used to treat septic shock, also DNA encoding it, for producing transgenic plant(s) resistant to fungal
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              Local Similarity
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101;
                                                                                                                                                                                                                                                                                                                                                              AAT10279
                                                                                                                                                                                                                                                                                                                                                                                                      Lee W;
                                                                    467
Conservative
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182
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13..467
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            14.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "mature protein"
58;
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           Score 314; DB 17;
Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide'
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Mismatches
                           DB 17;
                                                                                                                        can be used to treat diseases hock, to remove LPS from
143;
                        Length 467;
Indels
68;
Gaps
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                      The new enzyme is derived from alkaoplhilic Bacillus Sp. The enzyme acts on beta-1,3-glucans to form glucose and laminaribiose. It is stable over a wide pH range with opt. activity at weakly actidic pH and has good heat resistance.
                                                                                                      Heat resistant beta-1,3-glucanase alkali-compatible Bacillus sp.
                                                                                                                                                                                                                                                                                                                   Alkalophilic;
                                                                                                                                                                                                                                                                                                                                         Beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                         AAR11599;
                                                                                                                                                                                                                                                                                                                                                                                                                AAR11599 standard;
Sequence
                                                                                Claim 7; Fig 2; 11pp; Japanese
                                                                                                                                                     WPI; 1991-113290/16.
                                                                                                                                                                                                  20-JUL-1989;
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                                                                                                                                         AAQ11293
 261
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                                                                                                                                                                                                                                                                                                                      heat resistant.
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                                                                                                                    from
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Query Match Best Local Si Matches 100;

Similarity

13.8%;

Score 310; Pred. No. 1

DB 12; l.6e-21;

Length 261; Indels 15

154;

Gaps

17;

Conservative

35;

Mismatches

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ARESULT
AARP736

AARP736

AARP736

XX AARP

XX AARP

XX OG:

CO OG:

XX Beta

XX Beta

XX Pign

XX Pig
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                   DNA construct encoding enzyme with beta-1,3-glucanase activity useful for modifying or degrading beta-glucan contg. material a the prepn. of e.g. food colourants, flavourings and yeast extra
                                                                                                                                 WPI; 1996-222000/22.
N-PSDB; AAT29043.
                                                                                                                                                                                                            Asenjo JA,
Savva D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis; lytic enzyme; beta-glucan degradation; cell wall lysis; pigment; colorant; flavour; yeast extract; protoplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oerskovia beta-1,3-glucanase.
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                                                                                                                                                                                                                                                                                                                                             14-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-1995;
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225 --mlvdyvrvyg 234
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                                                                                                                                                                                                                                    Diers I,
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                                                                                                                                                                                                                                    Ferrer P,
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence (AAT29043) isolated from an O. xanthineolytica library. Recombinant beta-1,3-glucanase can be produced on a large scale using transformed host cells, esp. Bacillus subtilis DN1885 or Toc46. Protease-free beta-1,3-glucanase can be obtd. that is useful for lysing fungal cell walls, allowing recovery of intracellular proteins. The enzyme is also useful for the prepn. of protoplasts and for the prodn. of pigments, colorants, flavours, yeast extract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins. The enzymand for the prodn. cand pharmaceuticals.
                                                                         Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLG109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A novel beta-1,3-glucanase (AAR97362) from Oerskovia xanthineolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 42-43; 60pp; English.
 WO9811246-A2
                                                                                                                                                               erythrocyte;
                                                                                                                                                                              alpha-N-acetylgalactosaminidase;
                                                                                                                                                                                                                                                                       AAW56275;
                                                                                                                                                                                                                                                                                                    AAW56275 standard; Protein; 422
                                             Protein
                                                                                                                     Flavobacterium
                                                                                                                                                                                                              Flavobacterium
                                                                                                                                                                                                                                          18-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qpqfgrieariqiprgqgiwsafwmvganlpdtpwptsgeidimenvgnaphevhg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVWQDEFDYFDGAK-----WQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----tvh-gpgysgdn--gimgtyqhpqgwsfaddfhnfgidwtpgeitwlvd--gq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NINPOTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lawsdefdgaagsapnpdvwnhetgaggwanaelqnyttsrvnsal-dgq------ 116
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                                                                                                                                                                  transfusion; blood
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     -qwpgnpdattpfp--
                                                                                                                     keratolyticus
                                                                                                                                                                                                           keratolyticus endo-beta-galactosidase (ENDO-A) protein
                                             /note= "Signal peptide"
47..422
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.2%; Score 296; DB 17; 25.7%; Pred. No. 4.2e-20; tive 36; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -gnlvital-----gesdgsy-----tsarlttqgnv 142
                             "F. keratolyticus ENDO-A protein"
                                                                                                                                                                typing reaction; keratan sulphate,
                                                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                endo-beta-galactosidase; ENDO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -vfdqpfflilnvaigg-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 134;
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PT DR XXX PT T T XXX PT XXX

antifungal agent;

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RESULT 10
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AC AAR679
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Best Local Similarity
Matches 103; Conserv
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     14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endo-beta-galactosidase (designated ENDO-A) protein. The ENDO-A protein can be used in conjugation with alpha-N-acetylgalactosaminidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Fig 2A-2B; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated endo-beta-galactosidase - from Flavobacterium keratolyticus, used particularly for de-antigenising human erythrocytes bearing Al antigen for blood transfusions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldstein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1996;
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                                                                   AAR67915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transfusion of type Al blood.
degrade keratan sulphate (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the Flavobacterium keratolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NYBL-) NEW YORK BLOOD CENTER INC
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                                                                                                                                                                                                                                                                                                   WFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNL 301
                                                                                                                                                                                                                                                                                                                                                                                                                            AGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPED-WVYGGWPRSGEI
                                                                                                                                                                                                                                  APFDQNFHFILNVAVG-GTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW
                                                                                                                                                                                                                                                                                                                                                                           DIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLFGEGFAFTDWDQYHIVWQDEFDY---FDGAKWQHEVTATGGGN---SEFQLY-TQDGA 62
                                                                                                                                                                                                                                                                             tmiwspndirfyv---nnsl--
                                                                                                                                                                                                                                                                                                                                             dsmehvnnesv-----myhtihngsvtnang---gstasksatynttd-ynly
                                                                                                                                                                                                                                                                                                                                                                                                           agdpvayhaggvksmgkfsmtygkvevrakftqgrgswpaiwmmpepatayggwpscgei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       llnattvattd---yeliwsdefnssggfdstkwsyadrgtvawnkymtslpayasqdgs 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1998-207405/18.
                                                                                                                                                                                 KWTWDDEGDNNAMQVDYIRVYK 382
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                                                                   standard;
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   (first entry)
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                                                                                                                                                 mqvdyvrvyk 288
                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 286.5; DB 19; 27.0%; Pred. No. 5.1e-19; tive 32; Mismatches 100;
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ81334 encodes AAR67915 a (1-3)-beta-D-glucan sensitive factors has a high affinity for the (1-3)-beta-D-glucan found in fungational walls. The protein is therefore useful for clinically diagnosing mycosis, and as an antifungal agent for the removal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Pages 23-32; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding a polypeptide comprising a tetrapeptide motif least once - which may be used as an antibacterial and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-1994;
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                                                                                                                                                                                                                                                             yt-----sarlktqfdkswkygkieakmaipsfrgvwvmfwmsgdntnyvrwpss 135
                                                                                                                                                                                                                                                                                                                                                              QDGANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCY 118
                                                                                                                                                                                                                              GEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLP----KHSDDWN
                                                                                                                                                                                                                                                                                                                                                                                         lvllccvvlhvgvariccshepkwqlvwsdeftngissdwefemgnglngwgnnelgyyr 61
                  FFDARGNWKWTWDDEGDNNAMQVDYIRVYK 382
                                                                 kiqggvngksafrnkvfvilnmaiggn---
                                                                                                                                 tngidyhiysvewnssivkwfvngn---
                                                                                                                                                                                               geidfie-----hrntnne-----kvrgtihw--
                                                                                                                                                                                                                                                                                            RTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRS 178
                                                                                               NPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK
                                                                                                                                                                YGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYEND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            85;
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1..19
/label- sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.3%;
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-myidyvrvyq 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 209; DB 16;
; Pred. No. 2.2e-11;
49; Mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sek1 N;
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                                                                                                                                                                                                                                                                                       AAR67917-R67919 are active fragments of AAR67915, a (1-3)-beta-D-glucan sensitive factor, they have a high affinity for the (1-3)-beta-D glucan found in fungal cell walls. The proteins are therefore useful for clinically diagnosing mycosis, and as antifungal agents for the
                                                                                                                                                                                                                                                                                                                                                             DNA encoding a polypeptide comprising a tetrapeptide motif least once - which may be used as an antibacterial and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-3)-beta-D-glucan sensitive factor glucanase domain antifungal agent; mycosis diagnosis.
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 40; 51pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-060996/08
                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR67918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR67918 standard; Protein;
                                                                                                                                                                                                                                                                                removal of
                                                                                                                                                                                                                                                                                                                                                      antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                         Iwanaga
                                                                                                                                                                                                                                                                                                                                                                                                                         (SEGK )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-3)-beta-D-glucan
                                                                                                                          141
                 315 AVGGTNGFIPDGCINRGGDPALOKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMO 374
                                                                       128
                                                                                         201
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                                                                                                                                                              81
                                                                                                                                                                                          GIQKMGSTMHWGPGWDDNRYWLTSLP----KHSDDWN-YGDNFHTFWFDWSPNGLRFFV
                                                                                                                   SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEEL 200
                                                                                                                                                                             aiggn--
                                                     DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                      ---kvrgtihw-----stpdgahahhnresntngidyhiysvewnssivkwfv 172
                                                                                                        swkygkieakmaipsfrgvwvmfwmsgdntnyvrwpssgeidfie-----hrntnne--
                                                                                                                                            -----takredydgfkyt-----sarlktqfdk
                                                                                                                                                              NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                  Similarity
79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEIKAGAKU KOGYO CO LTD.
                                                                                                                                                                                                                                                              233 AA;
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                          9.38;
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                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
                                                                                                                                                                                                                 Score 208; DB 16;
Pred. No. 6.7e-12;
5; Mismatches 98;
-wpgfdvadea----fpak-----
                                  ----qyfevkiqggvngksafrnkvfvilnm
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                                                                                                                                                                        Matches
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                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                         grucanase
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                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces
                                            147
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          198
                             166
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 7-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-113611/10.
N-PSDB; AAX01742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGTase; beta-1,3-glucanase.
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224 idyvrvyg
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                                                                                                                                                                                                                                                                                                                                            1 MRWTLVVL--CLLEGEGEAFT-------DWDQYHIVWQDEED-----YEDGA 38
EFLGIQKMGSTMHWG---PGWDDNRYWLTSLPKHSDDWNYGDNFHTFWEDWSPNG----
                                                        --veariqvpnvtgdaakgywpafwmlgapyrgdywnwpavgeldime-----
                                                                                                    VVVHAKMPV----GD---WLWPAIWML--PEDWYYGGWPRSGEIDIIETIGNRDFKNTGG 197
                                                                                                                                                                                GTDFMYNGVLDVWAMYGACTNTDNNGCYRTG----AAGDIPPAMSARVRTFQKYSFTHGR 146
                                                                                                                                                                                                                      dwry-atgtgypggpsnwgtgeietmtsnpenvsldgngnlritp----- 136
                                                                                                                                                                                                                                                            KWQHEVTATG-----GGNSEFQLYTQDGAN-SFVRDGKLFIKPTLLADNINPQTGAPF 90
                                                                                                                                                                                                                                                                                                  lrrtlvalagalalgag-altltgptasasvppppsgwtg---vfaddfdgpkgsgvdtg 92
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp. SGTase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
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                                                                                                                                                                                                                                                                                                                                                                                                         7.5%;
24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used for recombinant production
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 168.5; DB 2
Pred. No. 6.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Japanese.
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        108; Indels 195;
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20;
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Best Local
                                                                                                                             Matches
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                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                    The present invention relates to Mycobacterium tuberculosis secreted proteins (MTSP), where the polypeptide has M. tuberculosis specific antigenic and immunogenic properties. Compositions of the invention be useful for diagnosing Mycobacterium tuberculosis infection and as
                                                                                                                                                                                                                                                                              Claim 11;
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-007151/01
                                                                                                                                                                                                                                                                                                                                                                      Gennaro ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB52463;
                                                                                                                                                                                                                                                                                                       Novel Mycobacterium tuberculosis secreted polypeptides and polynucleotides useful in diagnosis, treatment and prophyl tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-1999;
04-MAY-1999;
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                                                                                                                                                                                                           vaccine against M.
             135
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                                                                                                                                        Local Similarity
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           RTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGNRDFK 193
                                                                           llfhdefdgpagsvpdpskwqvsnhrtpiknpvgfdrpqffgqyrdsrqnvfldg-----
                                                                                                     IVWQDEFD----YFDGAKWQ---HEV---TATGGGNSEFQLYTQDGANSFVRDGKLFIK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dhgffvilnvamgg--gf-pdaf---
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                                                        PTILIADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARV 134
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                                                                                                                                                                                                                                                                          Fig 1;
                                                                                                                                                                                      294 AA;
                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Gomez MJ;
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990S-0132503.
                                                                                                                                                                                                                                                                          60pp;
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                                                                                                                            43; Mismatches
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                                                                                                                                       Score 138.5; DB:
Pred. No. 3.6e-05
NEW
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                                                                                                                                                 DB 22;
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Indels
                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                            prophylaxis
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Query Match
Best Local S
Matches 86
                                                                                                                            This polypeptide is immunologically reactive with antibodies raised against a pure endo-1,3(4)-beta-glucanase from T. harzianum CBS 243.71. Using this sequence, the protein may be expressed recombinantly in transformed host cells, particularly Aspergillus oryzae or Aspergillus niger. Typical applications of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast; fungus; enzyme; endo-beta-glucanase; EC-3.2.1.6; hydrolase; endo-1,3(4)-beta-glucanase; beta-glucan degradation; hydrolysis; detergent; surfactant; fungicide; antifungal; cleaning.
                                                                                                                                                                                                             Claim 1; Page 40;
                                                                                                                                                                                                                                     DNA encoding endo-beta-glucanase from Trichoderma harzianum useful, e.g., in food processing, as antifungal agent, in cl compsns., etc.
                                                                                                                                                                                                                                                                                         WPI; 19
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trichoderma
                                                              Sequence
                                                                                       recombinantly produced protein are preparation of and yeast extracts, brewing, wine and press-juice foods and feeds, as antifungal agents, etc.
                                                                                                                                                                                                                                                                                                                             Kauppinen
                                                                                                                                                                                                                                                                                                                              Andersen LN,
Kauppinen MS,
                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichoderma harzianum CBS 243.71.
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DB; AAT09876.
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Kofod LV, Olsen
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sen HS;
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Conservative

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109;

Indels

151;

Gaps

23;

Similarity

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RESULT 15
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XX Phaff1
               The present sequence represents the filamentous fungus Phaffia rhodozyma (CBS No. 6938) endo-1,3(4) beta-glucanase sequence. The enzyme may be used for modification or degradation of material which contains beta-glucan. Therefore the enzyme is claimed to be useful in, e.g. brewing, wine-making, preparation of protoplasts from yeasts, or preparation of pigments, colourants or flavourants. The enzyme is also claimed to be useful in the preparation of
                                                                                                                                                                                                              Claim 2; Pages 27-28; 36pp; English.
                                                                                                                                                                                                                                                            Enzyme with endo-1,3(4)-beta-glucanase activity - which is useful in, e.g. brewing, wine-making, preparation of protoplasts from yeasts, or preparation of pigments, colourants or flavourants
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N-PSDB; AAV59143.
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 inttfcg---
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               LNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWY 346
                                              naipaditqgvplp-----etwgtpm----gnfp---stscepfkffkdhhti
                                                                        NQALLD----VPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFD--QNFHFI
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---dwansdww 377
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Search completed: October 11, Job time: 202 sec 2001, 15:51:39

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Run

Title: Perfect score:

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Post-processing: Minimum Match 0%
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-712-072C-4
US-08-712-072C-2
US-08-712-072C-2
US-08-712-072C-2
US-08-7130-945-2
US-09-985-458-3
US-09-986-690-1
US-09-16-295-2
US-09-120-365-5
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Result No.

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Query Match

351.5 351.5 351.5 344.5 307

98.5 90.5 90.5 90.5 89.5 89.5

Patent

286.5 272.5 208 208 129.5 112.5 110.1 100 100

ALIGNMENTS

Minimum Maximum

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Database

JS-08-712-072C-3 Sequence 3. Application HS/08712072C
MATION:
TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
R OF SEQUENCES:
33
EE: Amste
T: 90
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TOOLS
SLE FORM:
PE: 3.5
IBM PC C
SOFTWARE: ASCIT
LICAT
CATION NUMBER
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
ian, Eliza
TRATION NUMBER: 39,9
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
E: (212) 697-5995
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CHARACTERIST
H: 321
ATTO MILLIO MOLLO
TOPOLOGY: linear
PE:
HYPOTHETICAL: NO
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PE
ORGANISM: el3b, Bacillus circulars
JS-08-712-072C-3

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                  TELEFAX: (617) 248-71 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING TITLE OF INVENTION: THEREOF
                                                              REFERENCE/DOCKET NUMBER: FJ
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MUTA, TATSUSHI
APPLICANT: SEKI, NORIAKI
APPLICANT: ODA, TOSHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
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                                                                                                                                               APPLICATION NUMBER: FILING DATE: 28-FEI CLASSIFICATION: 53/
                                                                                                                                                                                                                                                                                                                                                   CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
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                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                     ZIP: 02109
                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ ADDRESSEE: THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KWTWDDEGDNNAMQVDYIRVYK 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLIWQDEFNETTLDTSKWNYFTGYYLNNDPATWGWGNAELQHYTNSTQNVYVQDGKLNIK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFDQNFHFILNVAVGGT--NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIKWYVDGKFFYKVTNQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVYGTWAASGEIDVMEARGRLPGSV 205
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                                                   (617)
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                                                                                                                                                            UMBER: US/08/392,828C
28-FEB-1995
                                248-7100
                                                  248-7000
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26.2%;
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Pred. No. 2.8e-28;
6; Mismatches 86
                                                                                                                                                                                                                    Version
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Matches
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                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                          TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT
NUMBER OF SEQUENCE: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
                                  SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                       COUNTRY: US
ZIP: 02110
                                                                                                                                                                                         STREET: 125 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 A-----MNDSKSFPQDP-----NRYAQYS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
FILING DATE:
                  APPLICATION NUMBER:
                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 NLIWQDEFNGTTLDTSKWNYETGYYLNNDPATWGWGNAELQHYTNSTQNVYVQDGKLNIK 63
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                                                                                                                                                                                                             125 HIGH STREET
                                                                                                                                                         USA
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SEKI, NORIAKI
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                                                      Release #1.0,
                   US/09/330,945
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Pred. No. 7.6e-28;
44; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NASDIPA--
                                                      Version
                                                      #1
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COMPUTER:

IBM PC COMPATIBLE

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LOCATION: 1..262
OTHER INFORMATION: /note- "BG1 A1 SEQUENCE (FIGURE --09-330-945-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                      Sequence 4, Application US/08712072C Patent No. 5925541
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 248-7000
COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
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                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                          VOLUME OF INVENTION: ENDO-BETA-GALACTOSIDASE OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 NTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVYGTWAASGEIDVMEARGRLPGSV 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/119,995 FILING DATE:
                                   COUNTRY: UZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                      STATE:
                                                                                       CITY: New York
                                                                                                    STREET:
                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 NLIWQDEFNGTTLDTSKWNYETGYYLNNDPATWGWGNAELQHYTNSTQNVYVQDGKLNIK 63
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                                                                                                                                                                                                                                                                                                                                                                                              PFDEPFYLIMNLAVGGNFDGGRTP----NASDIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWN-----YGDNFHTFWFDWSPN 248
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                                                                    XX
                                                                                                    E: Amster, Rothstein & Ebenstein 90 Park Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 351.5; DB 3
Pred. No. 7.6e-28;
4; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SSGGDYHFPEGQTFANDYHVYSVVWEED 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----QWYSTAAPNNPN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SGKI 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
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                                                                                       US-08-824-707-2
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                Sequence 2, Applicating Patent No. 5919688
GENERAL INFORMATION:
APPLICANT: Ferrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: TWX 710-581-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                              258
                                                                                                                                                                                                                                                                                                           183
                                                                                                                                                                                                335 ALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                     275 WYDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAYGGTNGFIPDGCINRGGDP 334
                                                                                                                                                                                                                                                                                                                                                                                                                  170 WVYGG--WPRSGEIDIIETIG-NRD-----FKNTGGEFLGIQKMGSTMHWGPGWDDNRY 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 TNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPED 169
                                                                                                                                                                                                                                                                                                                                           221 WLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDE-----NQALLDVPYPLIDANPW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 697-3999
TELEPAX: (212) 286-0854 or 286-0082
TELEPAX: TWX 710-581-4766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bogosian, Elizabeth REGISTRATION NUMBER: 39,9: REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
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SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRWTLVVLCLLFGEGFAFTD-----WDQYHIVWQDEFDYF---DGAKWQHEVTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSEFQLYTQDG-ANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGAC 109
                                                                                                                                                                                                                                                                                                                                                                                QTYGSAYWPDNGEIDIMEHVGFNPDVVHGTVHTKAYNHLLGTQRGGS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQELQYYTRARIENARVGGGVLIIEA----RHEPYEGREY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRRTAFILSVLIGCSMLGSDRSDKAPHWE---LVWSDEFDYSGLPDPEKWDYDVGGHGWG
                                                                                                                                                                                                                                                                                                           --IRVPTARTD-----FHVYAIEWTPEEIRWFVDDSLYYRFPNERLTD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                     Application US/08824707
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Ferrer, Pau
Diers, Ivan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.4%; Score 344.5; DB 2; 27.5%; Pred. No. 4.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MS-DOS
                                                                                                                                                             -EAFPAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TSARLVTRGKASWTYGRFEIRARLPSGRGTWPAIWMLPDR 135
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                                                                                                                                                              -LVVDYVRVYR 273
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                                                                                                                                                                                                                                                                                                           -PEADWRHW
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APPLICANT:

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RESULT 6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acid
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NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                 380 VY 381
                                                                                                                                                                                                                                                                                                                  199 -----TVH-GPGYSGDN--GIMGTYQHPQGWSFADDFHTFGIDWTPGEITWLVD--GQ 246
                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                                                                                                                                                                                                                                               143 QPQFGRIEARIQIPRGQGIWSAFWMVGANLPDTPWPTSGEIDIMENVGNAPHEVHG---- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                    141 SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 --
                                                                          300 VY 301
                                                                                                                                                                                               320 NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIR 379
                                                                                                                                                                                                                                                                           260 ALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 IVWQDEFDYFDGAK-----WQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/824,707 FILING DATE: 14-April-1997 CLASSIFICATION: 435
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                         GIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAWSDEFDGAAGSAPNPDVWNHETGAGGWGNAELQNYTTSRVNSAL-DGQ------ 116
                                                                                                                                                                                                                                        EYHRVTTADVGANQW----
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10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: No. 59196880 No. 5919688disk of No. 5919688th America, 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 amino acids
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Cayva, Demitris
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                                                                                                                                                          -QWPGNPDATTPFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 307; DB 2; Length 306; 26.2%; Pred. No. 3.1e-23; ative 36; Mismatches 97; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 5919688el enzyme with beta-1,3-glucanase activity
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                                                                                                                                                          -QQMKVDYVR 299
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                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Jack Gold
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-SEP-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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302 APFDQNFHFILNVAVG-GTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW 360
                                                                                                               136 DSMEHVNNESV------MYHTIHNGSVTNANG---GSTASKSATYNTTD-YNLY 179
                                                                                                                                                     182 DIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTF 241
                                                                                                                                                                                                                             123 AGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPED-WVYGGWPRSGEI 181
                                                                          242 WFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNL 301
                                                                                                                                                                                          76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bogosian, Elizabeth
REGISTRATION NUMBER: 39,91
REFERENCE/DOCKET NUMBER: 6
                                                                                                                                                                                                                                                                   65 NLVLR-----
                                                                                                                                                                                                                                                                                                          63 NSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGA 122
                                                                                                                                                                                                                                                                                                                                                                               10 LLFGEGFAFTDWDQYHIVWQDEFDY---FDGAKWQHEVTATGGGN---SEFQLY-TQDGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC OPERATING SYSTEM:
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STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                       TMIWSPNDIRFYV---NNSL-
                                                                                                                                                                                          AGDPVAYHAGGVKSMGKFSMTYGKVEVRAKFTQGRGSWPAIWMMPEPATAYGGWPSCGEI 135
                                                                                                                                                                                                                                                                                                                                             LLNATTVATTD---YELIWSDEFNSSGGFDSTKWSYADRGTVAWNKYMTSLPAYASQDGS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 amino acids
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VENTION: ENDO-BETA-GALACTOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 3.
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                                   -QYTYARVSGGGTQQ 210
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MOLECULE TYPE: pe
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRACMENT TYPE: N-
; ORIGINAL SOURCE:
US-08-712-072C-2
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                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                              Matches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Elizabeth A.
REGISTRATION NUMBER: 39,911
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 INC
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   109
                               127 PPAMSARVRTFQKYSFTHGRVVVHAK-----MPV---GDWLWPAIWMLPED-WVYGGWPR 177
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                                                                                                                                                            10 LLFGEGFAFTDWDQYHIVWQDEFDY---FDGAKWQHEVTATGGGNSEFQLYTQDGANSFV 66
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SOFTWARE: ASCII
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                                                                                              RDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI 126
                                                                                                                              LLNATTVATTD---YELIWSDEFNSSGGFDSTKWSYADRGTVAWNK--YMTSQDGSNLVL 99
PVAYHAGGVKSMKFSMTYGKVEVRAKFTGVSLPAYAQGRGSWPAIWMMPEPATAYGGWPS
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                                                                                                                                                                                                                                                                                                                                                                                                                        422 amino acids
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                                                                                                                                                                                                                                                                                                             N-terminal
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DN: ENDO-BETA-GALACTOSIDASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697-5995
                                                                                                                                                                                            12.2%; Score 272.5; DB 2 27.2%; Pred. No. 1.6e-19; tive 29; Mismatches 97
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                                                                                                                                                                                                                          Length 422;
                                                                                                                                                                                              Indels 155;
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                                                                                                                                     Query Match
Best Local S
Matches 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 654 amino acids
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: CAMPBELL, PAULA A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 YNLYTMIWSPNDIRFYV---NNSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 02109
56
                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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                                81
                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                   23 QYHIVWQDEFDYFDGAKWQHEV--TATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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                                                                  KWQLVWSDEFTNGISSDWEFEMGNGLNGWGNNELQYYRRE--NAQVEGGKLVI----- 55
                                NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
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                                                                                                                                  ch 9.3%; Score 208; DB 1; Length 654; I Similarity 21.5%; Pred. No. 1e-12; 79; Conservative 45; Mismatches 98; Indels 1
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SEKI, NORIAKI
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-TAKREDYDGFKYT----
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                                                                                                                                       Indels 146;
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-SARLKTQFDK 78
                                                                                                                                       Gaps
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                                                                                 ; MOLECULE TYPE: protein US-09-330-945-2
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Query Match 9.:
Best Local Similarity 21.:
Matches 79; Conservative
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                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acid
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SINUMBER OF SEQUENCES: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                      TOPOLOGY:
                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FJN-032DV
                                                                                                                                                                                                                                                                                        NAME: PITCHER, EDMUND
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: BOSTON
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    Application US/09330945
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MUTA, TATSUSHI
SEKI, NORIAKI
ODA, TOSHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 HIGH STREET
                                                                                                                                                  654 amino acids
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                                                                                                                      linear
                                                                                                                                                                                                                      (617) 248-7000
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248-7100
240: 2:
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Score 208; DB 3; Length 654; Pred. No. 1e-12; 5; Mismatches 98; Indels 1
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   Indels 146;
   Gaps
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US-08-737-526-4
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APPLICANT: Kofod, Lene Venke
                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kauppinen, Markus Sakarı
APPLICANT: Kauppinen, Markus Sakarı
APPLICANT: Christgau, Stephan
                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/737,526 FILING DATE: 08-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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:||:||:
227 IDYVRVYQ 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 GIQKMGSTMHWGPGWDDNRYWLTSLP-----KHSDDWN-YGDNFHTFWFDWSPNGLRFFV 254
                                                   LENGTH:
TYPE: a
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                                                                                                                             TELEPHONE: 212-00.
TELEPHONE: 212-878-9655
                                                                                                                                                                                                    NAME: Valeta, Gregg A REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON OPERATING SYSTEM: SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                 STRANDEDNESS:
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             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
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                                                                                                                                                                                                        4174.204-US
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US-09-098-580-4
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09098580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,526
FILING DATE: 08-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
            REFERENCE/DOCKET NUMBER: 41 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400960 No. 6140096d1sk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: An Enzyme With Endo-1,3(4)-B-Glucanase TITLE OF INVENTION: Activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                NAME: Valeta, Gregg A REGISTRATION NUMBER:
                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARGNWKWTWDDEGDNNAMQVDYIRVY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V---DGQATGHGTLHCDVYPGGICNEGNGI-GGPVNIANVNDWHAWRVEIDRTPSSW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYTFTPAAGKVTRLEAAIRFGSNAQANKQGIWPAFWMLGDSLRQPGGSWPNCGEIDIMET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --QLVPWRDSSKGT-----STFGGWT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADNINPQTGAPEGTDEMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNLVWTDTFAGNGGTSPNQNNW-NIITGNLNVNAEQETYSSSTANVQLSGGS----TL-
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                                                                                                                                                                                                                                                                                                                                                              New York
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                                                                                                                                                                                                                                                                                                                                                                           405 Lexington Avenue
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Christgau, Stephan
                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kofod, Lene Venke
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212-867-0123
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22.0%; Pred. No. 3.1
                                                                                                                                                                                      US/09/098,580
                   35,127
PR: 4174.204-US
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                                                                                                                                                                                                                                                                                                                                                                                              6140096th America, Inc
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Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Applicati Patent No. 5344777 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER: IBM PC compat.
OPERATING SYSTEM: MS DO:
SOFTWARE: ASCII FOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                                                                                                                                                                        APPLICANT: Kawamura,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                        COUNTRY:
                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V---DGQATGHGTLHCDYYPGGICNEGNGI-GGPVNIANVNDWHAWRVEIDRTPSSW---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYSFT--HGRVV-VHAKMPVG------DWLWPAIWMLPEDWVY--GGWPRSGEIDIIET 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --QLVPWRDSSKGT-----STFGGWT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---NNIA--HSPLFFILNVAVGG--
                                                                                                                10016-2088
                                                                                                                                                                New York
                                                                                                                                                                                                                                                                         r: Okumura, Hajime and
I: Kawamura, Yoshiya
INVENTION: Structural Gene of Membrane-Bound
INVENTION: Alcohol Dehydrogenase Complex, Plasmid
                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/07985458
                                                                                                                                                                               600 Third Avenue
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Fukaya, Masahiro;
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                                               MS DOS
                                                                                                                                                                                                                                            Bacteria
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    US/07/985,458
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                                                                (NEC PC-9801 ES)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19921203
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,22
FILING DATE: 20-FEB-1991
APPLICATION NUMBER: 73440/1990
FILING DATE: 26-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
                 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION
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                                               379 AKTGEFI-----SGKNYVYVNWASGLDPKTG----RPIYNPDALYTLTGKEWYGIPGD 427
                                                                                                                                                                                                                                                       212
                                                                                                                                                                                 259 KAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYRSEGKGDNLFLG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ritle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
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MG----STMHWGPGWDDNRYWLTSLP-----
                                                                                                                                                                                                                                                      GNGGSEF------GARGFVSAFDAETGKVDWRFFTVP-----NPKNEPDAASDSVLMN 258
                                                                                                                                                                                                                                                                                     GGGNSEFQLYTQDGANSFVR------DGKLFIKPTLLADNINPQTGAPFGTD-FMYN 97
                                                                                MPVGDWLWPAIWMLPEDWVYGGW-----PRSGEIDIIETIGNRD--FKNTGGEFLGIQ-K 204
                                                                                                              SIVALKPETGEYVWHFQETPMDQWDFTSDQQIMTLDLPINGETRHVIVHARKNGFFYIID 378
                                                                                                                                                 ---- IPPAMSARVRTFQ-----KYSFTHGR----
                                                                                                                                                                                                                  GVLDVWAMYGACTNTDNNGC----
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning and Sequencing of the Gene Cluster
Encoding Two Subunits of Membrane-Bound
Alcohol Dehydrogenase from Acetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                           292-300
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Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212)370-1622
                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochimica et Biophysica Acta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawamura, Yoshiya;
Nishiyama, Makoto;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okumura, Hajime;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takemura,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetobacter altoacetigenes
                                                                                                                                                                                                                                                                                                                                   5.0%;
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                                                                                                                                                                                                                                                                                                                     Score 112.5; DB 1;
Pred. No. 0.0062;
7; Mismatches 113;
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               ---KHSDDWNYGDNEHTEWED 244
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a molecular
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; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-286-690-10
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US-09-286-690-7
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                                                                                                                                                           Sequence 7, Application US/09286690 Patent No. 6103511
                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity 21.9%;
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                                               APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05 EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04 EARLIER APPLICATION NUMBER: PCT/US97/17811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Li, Xin-Liang APPLICANT: Ljungdahl, Lar APPLICANT: Chen, Huizhong
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CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05
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                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 55-96
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                                                                                                                                                                                                                                                                                                                                                                                                    229
                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TG-PTDGTPWDEIDI-------EFLG--KDTTKVQF-----NYYTNGVGNH 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLGEMRLSLTSPSYNKFDCGENRSVQTYGYGLYEVNMK---
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                                                                                                                                                                                                                                                                                                                      FWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFLSLSTFAASASAQTGGSFYEPFNNYN--TGLWQKADGYSNGNMFNC--TWRANNVSMT
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Pred. No. 0.0023;
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EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04

APPLICATION NUMBER: PCT/US97/17811

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LENGTH: 238;
TYPE: PRT;
ORGANISM: Bacillus polymyxa
US-09-286-690-7
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-10-03
                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Von Wettstein, Dietrich TITLE OF INVENTION: A Thermostable (1,3-1,4)-beta-Glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 QKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYG----DNEHTFWEDWSPNGLREFYDD-- 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 22.0%;
                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
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Hofemeister, Jurgen
Thomsen, Karl Kristian
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   NUMBER:
                                                                                            us 07/773,652
                                                                                                                                                                  us/08/103,998
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30307/123
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Pred. No. 0.0056;
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Search completed: October 11, 2001, 15:52:05 Job time: 208\ \text{sec}
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Best Local Similarity 20.6%;
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
                                                                                                  201 KIMMNLWNGTGVDDWLGSYNGVNP 224
                                                                                                                                       275 WYDFWEWG----KPWLPQYENDNP 294
                                                                                                                                                                                   146 YTNGAGNHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQLKHTATTQIP---
                                                                                                                                                                                                                                                                                                      207 --- STMHWGPGWDD-------NRYWLTSLPKHSDDW--
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                                                                                                                                                                                                                                                              86 EYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNY 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                       -FHTFWFDWSPNGLRFFVDDE---NQALLDVPYPLIDANPW 274
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Pred. No. 0.023;
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Post-processing: Minimum Match 0%
Maximum Match 10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
353
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Gapop 10.0 ,
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2240
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Compugen Ltd
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Million cell updates/sec
                                                  hypothetical prote
Avicelase III - As
Licheninase (EC 3.
neuraminidase - Vi
neuraminidase VC17
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probable beta-1-
probable glucanase
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hypothetical prote
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endo-1,4-beta-xyla
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glucan endo-1,3-be
                       probable beta-gluc
KRE6 protein - yea
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laminarinase - The
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mixed-linked gluca
probable phosphati
licheninase (EC 3.
                                         xyloglucan endo-1,
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                                                                                                                     endo-beta-N-acetyl
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licheninase (EC 3.
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GGVNYF--
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45	44	43	42	41	40	39	38	37	36	ω 5	3 4	ω ω	32	31	30
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4.4	4.4	4.4	4.4	4.4	4.5	4.5	.5	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7
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S60040	A29130	C86189	S41797	T49073	T06201	S71222	T44496	S23498	I40453	F71402	H84053	A29091	A36910	G64157	A49340
alpha-amylase (EC	beta-amylase (EC	protein T25N20.1:	cellulose 1,4-be	hypothetical prote	xyloglucan endo-1	xyloglucan endo-1	cellulose 1,4-beta	licheninase (EC 3.	licheninase (EC	xyloglucan endo-1	endo-beta-1,3-1,	licheninase (EC	xylanase, beta(1	probable organic	alcohol dehydrog

ALIGNMENTS

beta 1,3-glucanase (EC 3.2.1.-) precursor - sea urchin (Strongylocentrotus purpuratus C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 21-Jul-2000 C;Accession: JC6141; PC6037
C;Accession: JC6141; PC6037
C;Bacchman, E.S.; McClay, D.R.
R;Bacchman, E.S.; McClay, D.R.
A;Title: Molecular cloning of the first metazoan beta-1,3 glucanase from eggs of the efense enzymes in plants.
efense enzymes in plants.
effenywords: egg; glycosidase; hydrolase
F;120/Domain: signal sequence #status predicted <SIG>
F;21-499/Product: beta 1,3-glucanase #status predicted A;Molecule type: protein A;Residues: 21-40;197-209;329-344 <BA2> A;Experimental source: egg C;Comment: This enzyme functions in several extracellular activities including autoca A;Molecule type: mRNA A;Residues: 1-499 <BAC> A;Cross-references: GB:U49711; NID:g1488256; PIDN:AAC47235.1; A;Reference number: JC6141; MUID:96270625 A;Accession: JC6141 A; Accession: PC6037 143 THGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGI 202 :||: | ||: | || || ||: ||: || || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 179 LIFQEEFDSFNLDIWEHEMTAGGGGNWEFEYYTNNRSNSYVRDGKLFIKPTLTTDKL--- 235 Local Similarity DQMGSTMHWGPFWPLNGY ----PK----KYGRLEVEAKLPTGDWLWPAIWLLPKHNGYGEWPASGEIDLVESRGNADIKDADGLSAGV GGTNGFIPDGCINRGGD-----PALOKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNN 371 ----LLLNVDP-ATGFWDLG-----EFENDAPGIDNPWAYNPNKLTPFDQEFYLILNVAV DVPYPLIDANPWWVDFWEWGKPWLPQYEN-----DNPWAGGTN-LAPFDQNFHFILNVAV 316 ----GEGSLSSGTLDLWGSSPANLCTGNAWYGCSRTGSNDNLLNPIQSARLRTVESFSF 290 TGAPFGTDFMYNGVLDVWAMYGA--CTNTDNNGCYRTGAAGD-IPPAMSARVRTFQKYSF 142 Conservative ----GDGLTYTPA--KPWSNDS--PTASKDFWSDFNTWYPTWN--GEEA 476 31.8%; 42.7%; 48; Score 713; DB 2; Pred. No. 4.7e-50; Mismatches 88; ---THATKFYVDDE----Length 499; Indels <MAT> PID:g1488257 Gaps 350 431 381 15;

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A;Accession: PN0613
A;Molecule type: protein
A;Residues: 39-58 <YA2>
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T18265
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Biosci. Biotechnol. Biochem. 57, 1518-1525, 1993
A;Title: Structure of the 87-kDa beta-1,3-glucanase
A;Reference number: JN0772; MUID:94033858
A;Accession: JN0772
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submitted to the EMBL Data Library, July 1995 A; Reference number: 218848
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A;Accession: T18265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DhA;
A;Residues: 1-1324 <SCH>
A;Cross-references: EMBL:X89732; NID:g1143428; PID:GC:Genetics:
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C:Date: 07-Sep-1990 #sequence_revision
C:Accession: JQ0420 # Nakamura,
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C;Keywords: hydrolase; glycosidase
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F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-682/Product: beta-1,3-glucanase Al #status predic
                                                                                                                                                                                                                                             A; Experimental source: strain WL-12
C; Comment: This enzyme, together with chitinase,
                                                                                                                                                                                                                                                                                                      A; Accession: JQ0420
A; Molecule type: DNA
A; Residues: 1-682 < YAH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-1,3-glucanase Al precursor - Bacillus circulans
C;Species: Bacillus circulans
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                                   HIVWQDEFD--YFDGAKWQHEV-----TATGGGNSEFQLYTQDGANSFVRDGKLFIK 74
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26.2%;
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                                                                        Score 351.5; DB 2;
Pred. No. 1.1e-20;
4; Mismatches 89;
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135 507 195 507 195	**RYDKYSTHGRVVVHAKHPVGDWJAPALMALPEDWYTGGWPRSGEIDIETGNIDEKN 194 **RYDKLSLKTGNYDFRAKLPTGDVWPALMALPEDSVGTWAASGEIDVMEARGRIPGSV 566 ***ROZEFLAJONAGSTMENGGADDNEWALTSLEKKSDDW3***********************************
Db 484 AMNDSKSFPQDP-	AMNDSKSFPQDPNRYAQYSSGKI 506
484 A	SGKI
135	
507	
	YGDNEHTEWEDWSPN
SG	SSGGDYHFPEGQTFANDYHVYSVVWEED
GLRFFVDDE	
	A
	NASDIPA
	RVYK 382
70	
RESULT 5 \$48201 \$11cheninase (EC 3.2.1.73) p N;Alternate names: beta-glu C.Species: Rhodothermus mar	Rhodothermus mari do-beta-1,3-1,4-D-
C; Accession: S48201 R; Spilliaert, R.; Hreggvids	Kristjansson, J.K.; Eggertsson, G.; Palsdottir,
Cloning and cloning and cloning and cloning and clonical cloners. S482(lon: S482)	marinus gene, bglA, coding for a
A; Residues: 1-286 <spi> A; Cross-references: EMBL:U0 A; Experimental source: stra C; Genetics:</spi>	NID:g450182; PIDN:AAA60459.1; PID:g45018
;Keywords: glycosidase; ;1-30/Domain: signal ser ;31-286/Product: lichen	lase #status predicted < #status predicted <
Match Local Simi es 112;	Score 344.5; DB 2; Length 286; Pred. No. 1.4e-20; 37; Mismatches 96; Indels 163; Gaps
13	
51 70	
110	
170	FKNTGGEFLGIQKMGSTMHWGPGWDDNRY
146	
221 WLTSLPKHSDDWNYGD ; 193IRVPTARTD	NQALLDVPYPLIDANPW :
275	

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C; Keywords: glycoprotein; immune response F;1-17/Domain: signal sequence *status predicted <SIG>F;1-17/Domain: Signal sequence *status predicted protein *status predicted <MAT>F;18-467/Product: Gram-negative bacteria-binding protein *status predicted F;119,182/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lee, W.J.; Lee, J.D.; Kravchenko, V.V.; Ulevitch, R.J.; Brey, P.T. Proc. Natl. Acad. Sci. U.S.A. 93, 7888-7893, 1996
A;Title: Purification and molecular cloning of an inducible Gram-neg A;Reference number: JC6150; MUID:96353914
A;Accession: JC6150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gram-negative bacteria-binding protein precursor C;Species: Bombyx mori (silkworm)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997
C;Accession: JC6150; PC6039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
JC6150
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RESULT 7
B72428
Laminarinase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-19
C;Accession: B72428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 42-53; 56-83; 88-100 <LEE2>
A; Experimental source: fat body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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A; Residues: 1-467 < LEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comment: This is a soluble protein having affinity for the Gram-negative bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                                                                                                                                                              456
                                                                                                                                                                                                                                          371 NAMQVDYIRV 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 GGEFLGIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN-----RDFKNT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT 143
                                                                                                                                                                                                                                                                                        AAGGITEF-RDGSITSGG----VTKPW-----RDSARKASVHFWRHMSDWFPRWSQP---
                                                                                                                                                                                                                                                                                                                                                                                   DGEEWARVEAPRDAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFEEQFDSLDENVWQIEQYIPIYHPEYPFVSYQRNNLTVSTADGNLHI-----NAKLQ
                                                                                                                                                                                              -SLIVDFVKV 464
                                                                                                                                                                                                                                                                                                                                    AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN 370
                                                                                                                                                                                                                                                                                                                                                                                                                            DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VLYGGPIMDLECRENFLSTKRRDGTSWGDSFHTYSVQWTPDFIALSV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGTVEIRAKLPQGDWLYPEILLEPFLKKYGSMNYASGVVKIACARGNAELYSGPNDYSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-467 <LEE1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Mismatches 143;
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*sequence_revision 11-Jun-1999 #text_change

21-Jul-2000

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A49878

A49878

Coagulation factor G alpha chain precursor - horseshoe crab (Tachypleus tridentatus C;Species: Tachypleus tridentatus C;Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 18-Aug-2000 C;Accession: A49878

R;Seki, N; Muta, T; Oda, T; Iwaki, D.; Kuma, K.; Miyata, T.; Iwanaga, S. J. Biol. Chem. 269, 1370-1374, 1994

A;Title: Horseshoe crab (1,3) beta-D-glucan-sensitive coagulation factor G. A se A;Reference number: A49878; MUID:94117453

A;Accession: A49878

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-673 <SEK>
A;Cross-references: GB:D16622
C;Superfamily: Clostridium xylanase A repeat homology
C;Superfamily: Clostridium xylanase A repeat homology <CXA>
F;437-532/Domain: Clostridium xylanase A repeat homology <CXA>
F;575-670/Domain: Clostridium xylanase A repeat homology <CXA>
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C.M.
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A; Gene: TM0024
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A;Molecule type: DNA
A;Residues: 1-642 <ARN>
A;Cross:references: GB:AE001690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Evidence for lateral gene transfer between A;Reference number: A72200; MUID:99287316 A;Accession: B72428
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 Query Match
Best Local S
Matches 85
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97; Conserv
   similarity 21.8%;
85; Conservative
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    49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TAH-GPGYSGGASIGVAY---HLPEGVPD--F
Score 209; DB 2;
Pred. No. 3.6e-09;
9; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                        457
                                                                                                                                                                                                                                                                                                                                       horseshoe crab (Tachypleus tridentatus)
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                                 Length 673;
    Indels 150;
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submitted to the EMBL Data I
A; Reference number: Z21570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable secreted glucosidase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #tex
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A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T35164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source:
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                               GNLRITP-----QRDGAGNWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEIDFIE-----HRNTNNE-----KVRGTIHW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YT----
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                                                                        EIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWG--PGWDDNRYWLTSLPKHSDDWNYGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFDARGNWKWTWDDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIQGGVNGKSAFRNKVFVILNMAIGGN---
                                                    EIDIME---
                                                                                                                                                                                                                                                                                                           103;
                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:AL031107;
ce: strain A3(2)
                                                    ----NT----QGLNTVWSTLHCGTSPGGPCNE---TS------GIGGN
    -ggklrveariqvpnvtgaaakgywpafwmlgapyrgnywnwpgvg
                                                                                                                                                                                                                                                                                                                         8.0%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MYIDYVRVYQ 253
                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                         Pred. No. 5.6e
28; Mismatches
      -SPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA19944.1;
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A;Gene: SCOEDB:SC5A7.15c
C;Superfamily: Clostridium xylanase A repeat homology
F;361-464/Domain: Clostridium xylanase A repeat homology
                                                                                                                                                                                                          21 WDQYHIVWQDEFDYFDG----AKWQHEVTAT--GG----GNSEFQLYTQDGAN-SFVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVVL-CLLFGEGFA---FTDWDQYHIVWQDEFDYFDGAKWQHEV--TATGGGNSEFQLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLP----KHSDDWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDGANSFYRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCY 118
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                                                                                                                       GKLF1KPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGD1PP
                                                                                                                                                                     WTQ----VFADDFDGAAGSGVNTANWQYDTGTSYPGGPANWGTGEIETMTSSPSNVSLDGG
                    AMSARVRTFQKYSFTHGRVVVHAKMPV------GDWLWPAIWML--PEDWVYGGWPRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill, J.; Barrell, B.G.;
Library, July 1998
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5.6e-07;
эя
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                                                                                     -SGRIETKRADFEPP
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                                                                                                                                                                                                                                                                                                                                                                            <CXA>
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182
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282

237

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probable beta-1,3-glucanase (EC 3.2.1.-) - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Nov-1999
C;Accession: T17584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Note: A94L
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tatus: preliminary; translated from GB/EMBL/DDBJ .Olecule type: DNA .Residues: 1-364 <GRA> A; Residues: 1-364 <GRA> A; Cross-references: EMBL:U42580; NID:g4028896; PIDN A; Experimental source: specific host Chlorella stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
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R;Cole, S.T.; Brosch, R.; ; Connor, R.; Davies, R.; Rajandream, M.A.; Rogers,
                                            RESULT 11

D70525

D70525

probable beta-1 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_ch

C;Accession: D70525
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hes 85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              NGTTWNTI----RVEARLKAPRGPGVVGAFWMLPID--NSCFP---EIDIFETPYCERA
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                                                                                                                                                                                                        GNWKWTWDDEGDNNAMQVDYIRV
                                                                                                                                                                                                                                                                                                                                  WFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNL 301
                                                                                                                                                                                                                                                                                                                                                                 SMGTWYVNKDVPR-----GISKHGTTI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIET-----
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                                                                                                                                                                                                                                         NDTDAPYNRPFYIILNTSIGSAWGGIP
                                                                                                                                                                                                                                                                                                      AVEWNADY IAFYAGDAE - - - - - TPVFVT - - -
                                                                                                                                                                                                                                                                                                                                                                                             -IG----NRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGA-----AGDIPPAMSA 132
                                                                                                                                                                                                                                                        ----APFDQNEHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDAR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                            -VLDVDYVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.6%; Score 148; DB 2; Length 364; 22.2%; Pred. No. 0.00014; tive 40; Mismatches 108; Indels 1
Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D
Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;
J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares,
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Library, May
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                                                                                                                                                                                                          380
                                                              17-Jul-1998 #text_change 22-Oct-1999
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strain NC64A
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        , D.; Goruu.,
N.; Holroyd,
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 GAPFGTDEMYNGVLDVWAMYGACTNTDNNGCYRTG--AAGDIPPAMSA----
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A;Cross-references: EMBI
A;Experimental source: s
C;Genetics:
A;Gene: SPAC21B10.07
A;Map position: 2
                                                                                                                                                                                                                              C;Accession: T39920

R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; submitted to the EMBL Data Library, October 1997

A;Reference number: Z21891

A;Accession: T39920

A;Accession: T39920
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.;
A;Title: Deciphering the biology of Mycobacterium tuberculosis fi
A;Reference number: A70500; MUID:98295987
A;Accession: D70525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-294 <COL>
                                                                                                                                                                                                                                                                                                         probable glucanase precursor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39920
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A;Experimental source: strain I
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                                                                                                                                                                               A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-419 <MCD>
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Best Local S
Matches 80
                  Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        -MLVDWVRVF
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 56; Conserv
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   Conservative
                                                                                                                                               EMBL: AL121794; PIDN: CAB57923.1; ce: strain 972h-; cosmid c21B10
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                5.9%;
23.1%;
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21.6%;
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H37Rv
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31;
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                  Score 132; DB 2;
Pred. No. 0.0034;
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   Mismatches
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                                   Length 419;
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A; Accession: A75132
A; Status: preliminary
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A;Residues: 1-1144 <KAW>
A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49770.1; PID:e151566
A;Experimental source: strain Orsay
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WYNDAMRKFFDARGNWKWTWDDEGDNNAM------
                                                                ----DGNEWITGTNLNSVGEYAY-----IGGDNGI---
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                                                                                                            WLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGD
                                                                                                                                                        YWPDYGVAIDVNPGSGIGGTYDPWAKKIYFSGTYLPDYIIYAEAQDGALTWVGLCKW----
                                                                                                                                                                                                                                                NFIEISLTKVIDGNLDDWNKAELVAQGVPSGIEGANLDRLYVSWDSNYLYIAIKTNNTAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EFQLYTQDGANSEVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYG
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C;Superfamily: Bacillus subtilis hypothetical protein
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A;Experimental source: strain 168
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C;Date: 05-Dec-1997 #sequence_revision:05-Dec-1997 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: B69798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bec.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: B69798
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B69798
C:Species: Bacillus subtilis
C:Species: Bacillus subtilis
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 DPTGIA-NTNEISLACFSHMPSDEVLNALADKWQAPPLIVCEPDVY-----YES
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    ----KWTWDD 366
                                              ----INCLKRLPLRLLSGPTFEYDPATSMLHHMGDGIAGGYHMIIAFGAPQVWMELA
                                                                                                                                   DADYALVKTDPMRA-FYEKGKH--PTHARTGPDWAAFCSNWLAEWERTENSEYLKKIETG
                                                                                                                                                                             DVPYPLIDANPWWVDFWEWGKPWLPQYENDNP-WAGGTN--LAPFD--QNFHFILNVAVG
                                                                                                                                                                                                                           NVVHWGCGCKEARISMAGL:
                                                                                                                                                                                                                                                                STMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALL----
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                                                                                                                                                                                                                                                                                                                                                          ---GDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIG--NRDFKNTG----GEFLGIQKMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLRYFFEKYPSALEITGLAGSRPKMTIWLWPPDGEAMDLRHYTGNTHVASAYEGFDEMRS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAHGTQNAVWDDVKIV-QDSSDHYSLSKRTGKDYAWVGMLHGSRAKGVCYAGGKNGGVAL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ALGGMPEKIAIIAWVAGNEDGNSAVDTLPVDPSIDYSNI
                                                                                       GTNGFIPDGCINR-----GG-----DPALQKPWSNGDWYNDAMRKF--FDARGNW----
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Pred. No. 0.029;
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A;Molecule type: DNA
A;Molecule type: CHA
A;Residues: 1-878 <STO>
A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04504.1; GSPDB:GN0C
A;Experimental source: strain C-125
C:Genetics:
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Search completed: October 11, 2001, 15:55:28 Job time: 286 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ene: BH0785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 ----PK--VYGGQE-----EWYDKMLVRGEDGSFPAADKLLEVAEYYGFDGWFINQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 AIWMLPEDWYYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTM-HWG-PGWDDNR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 MV-----YWAGSAGEGIITPPS------GDVIDAAHRNGVPILGNVFFP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 CTNTDNNGCYRTGAAGD---IPPAMSARVRTFQKYSFTHGRVVVHAK---MPV-GDWLWP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               726 ELLDDWEWED 735
                                                                                                                                                                                                                                                                                                                                                                                   196 ETEGGTPETAKDMQEFLLYLQENKPEGMHIMWYDSMISNGDIRWQNYLTDENAMFFQAGN 255
                                                                                                                                                  309 QVFPE----GGEPHTSLGIYRPDWAFKSTDTMRDFYD 341
                                                                                                                                                                                                            324 --- PDGCINRGGDPALQKPWSNGDW---YNDAMRKFFD 355
                                                                                                                                                                                                                                                                                                                                                                                                                                    220 YWLTSLPKHSDDW------NYGDNFHTFWFD--WSPNGLRF--FVDDENQALLDVPY 266
                                                                                                                                                                                                                                                                      256 RKY-ADSMFLNFW-W---WNHSQERSKQKAASLGRSPYD--LYAGIDVEANGTNTYVNWQ 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 SEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQT-GAPF--GTDFMYNGVLDVWAMYGA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 VLILVLLPSQGFASQPESSYWYPETLLDWSPETD--PDARFNRSSIPLREREV----- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LVVLCLLFGEGFAFTDWDQYH-----IVWQDEFDYFDGAKW--------QHEVTATGGGN 51
                                                                                                                                                                                                                                                                                                       PLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFI--- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LYTVNDTQQ--TDAKL----VALSALNPNTSGVPSQGGNEFFAN-TFGFWQYVDL 112
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Result
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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FUNG_HAEIN
SKN1_CANALL
XYNX_CLOTM
                 SKN1_YEAST
BRU1_SOYBN
MOKB_SCHPO
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MYCO_STRCI
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Compugen Ltd.
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Best Local Similarity
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15.7%; 26.2%;

Score 351.5; DB 1; pred. No. 1.4e-21; 44; Mismatches 89;

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Gaps

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P45798;
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MEDITINE-95010084; PubMed-7925416;
Spilliaert R., Hreggvidsson G.O.,
Eggertsson G., Palsdottir A.;
"Cloning and sequencing of a Rhodo
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01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update
ENDO-1,3-1,4-BETA-GLYCANASE EXSH (EC 3.2.1.
BLOSTYNTHESIS PROTEIN EXSH):
                       depolymerize nascent succinoglycan chains.";
proc. Natl. Acad. Sci. U.S.A. 95:4912-4917(1998).
-i- FUNCTION: CLEAVES HIGH MOLECULAR WEIGHT SUCCINOGLYCAN TO YIELD I SUCCINOGLYCAN, DYNAMICALLY REGULATE THE MOLECULAR WEIGHT DISTRIBUTION OF SUCCINOGLYCAN BY CLEAVING NASCENT SUCCINOGLYCAN ONLY DURING A LIMITED PERIOD AFTER ITS SYNTHESIS, PERHAPS BEFORE
                                                                                                                                                                                                                                                                                                                                                                                                        033680;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHIME
                                                                                                      CHARACTERIZATION.
MEDLINE-98226741; PubMed-9560202;
York G.M., Walker G.C.;
"The Rhizobium meliloti ExoK and ExsH glycanases
                                                                                                                                                                                    "The Rhizobium meliloti exoK gene and prsD/prsE/exsH components of independent degradative pathways which production of low-molecular-weight succinoglycan.";
                                                                                                                                                                                                                                                                                                             Rhizobium meliloti (Sinorhizobium meliloti) Plasmid pSymB (megaplasmid 2).
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
York G.M., Walker G.C.;
                                                                                                                                                                                                                                                                                                                                         EXSH.
                                                                                                                                                                                                                                                                                   Rhizobiaceae;
                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EXSH_RHIME
                                                                                                                                                              Mol. Microbiol.
                                                                                                                                                                                                                                                                      NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WVYGG--WPRSGEIDIIETIG-NRD-----FKNTGGEFLGIQKMGSTMHWGPGWDDNRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDE-----NQALLDVPYPLIDANPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTYGSAYWPDNGEIDIMEHVGFNPDVVHGTVHTKAYNHLLGTQRGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIDNINGCYRTGAAGDIPPAMSARVRIFQKYSFIHGRVVVHAKMPVGDWLWPAIWMLPED 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSEFQLYTQDG-ANSFYRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGAC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRRTAFLLSVLIGCSMLGSDRSDKAPHWE----LVWSDEFDYSGLPDPEKWDYDVGGHGWG
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112; Conserv
               UNDERGOES A TIME-DEPENDENT
                                                                                                                                                                                                                                                                                                            pSymB
                                                                                                                                                                                                                                                                                              SymB (megaplasmid Proteobacteria; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158
163
286
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                                                                                                                                                                                                                                                                                   Sinorhizobium
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
STATE
                                                                                                                                                                           25:117-134(1997).
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163
33145
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27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W.
                                                                                                                                                                                                                                                                                              alpha
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PROTON DONOR (BY SIMILARITY);
7215C33624135191 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                 subdivision;
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               CHANGE
                                                                                                                                                                                                                                                                                                                                                                 n update)
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               STI
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                                                                                                                                                                                                                                                                                                                                                                  (SUCCINOGLYCAN
                                                                                                         specifically
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                                                                                                                                                                                                    genes encode contribute to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283
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                                                                                                                                                                                                                                                                                               group;
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                                                                    EME
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RESULT 4

EGLC_RHME
ID EGLC_R
AC Q9Z3Q2
DT 30-MAY
DT 01-OCT
DE BIOSYN
GN EGLC.
OS Rhizob
OG Plasmi
OC Bacter
OC Rhizob
OX NCBLT
RN [1]
RP SEQUEN
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Best Local 9
                                                                                                                                               30-MAY-2000
30-MAY-2000
01-OCT-2000
ENDO-1,3-1,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXOPOLYSACCHARIDE SYNTHESIS; Glycosidase; DOMALN 275 465 CATALTRIC. ACT_SITE 349 349 NUCLEOPHILE (PROTON DONOR PROTON DONOR CENTRAL SEQUENCE 465 AA; 50286 MW; 6C8482366ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01034; GLYCOSYL_HYDROL_F16; FALSE_NEG. PROSITE; PS00330; HEMOLYSIN_CALCIUM; FALSE_NEG.
   SEQUENCE FROM N.A.
                                NCBI_TaxID=382;
                                                                                                                                  BIOSYNTHESIS
                                                                                                                                                                                                                                 EGLC_RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U89164; AAB64093.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM.
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320
                                                                                                                                                                                                                                                                                                                    442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: SECRETED. PROBABLY BY A TYPE-III SECRETION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: EXOPOLYSACCHARIDE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQT 86
                                                                                                                                                                                                                                                                                                                  GL----
                                                                                                                                                                                                                                                                                                                                               GCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRVY
                                                                                                                                                                                                                                                                                                                                                                                                              YPLIDANEWWVDEWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IATVH -- SNETGSRTSIENSVKVAD -- -- ASGFHTYGVLWTEEEIVWYFDDAAIARADTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFEMRADMPDDQGVWPAFWLLPAD---GSWP--PELDVVEMRGQD--SNT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWDAKF----YEPTA---SYNPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00722; Glyco_hydro_16; 1.
PF00353; hemolysinCabind; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001343;
                                                                                                                                              0 (Rel. 39, Created)
0 (Rel. 39, Last sequence update)
0 (Rel. 40, Last annotation update)
4-BETA-GLYCANASE EGLC (EC 3.2.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                PROTEIN EGLC).
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%;
21.6%;
                                                                                                                                                                                                                                                                                                                                                                                 --- YMY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
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PROTON DONOR (BY SIMILARITY);
6C8482366E9E8CA8 CRC64;
                                                                                                                                                                                                                                   PRT;
                                                                  subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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dase; Hydrolase; Plasmid.
                                                                                                                                                                                                                                 465
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                                                               Rhizobiaceae group;
                                                                                                                                                   (SUCCINOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                ---MLVNLAVGGIAGTPRD
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Best Local
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Pfam; PF00353; hemolysinCabind; 1.
PRINTS; PR00313; CABNONGRPT.
PROSITE; PS01034, GLYCOSYL_HYDROL_F16; FALSE_NEG.
PROSITE; PS01034; HEMOLYSIN_CALCIOM; FALSE_NEG.
PROSITE; PS00330; HEMOLYSIN_CALCIOM; FALSE_NEG.
PROSITE; PS00330; HEMOLYSIN_CALCIOM; FALSE_NEG.
PROSITE; PS01034; GLYCOSIDASe; Hydrolase; Plasm Exopolysaccharide synthesis; Glycosidase; Hydrolase; Hydrolase; Plasm Exopolysaccharide synthesis; Glycosidase; Hydrolase; Hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ225896; CAB38101.1;
InterPro; IPR000757; -.
InterPro; IPR001343; -.
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MEDLINE=99413305; PubMed=10485295;
447
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SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ð---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQTGA-PFGTDFMYNGVLDVWAMYGA- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAFTDWDQYHI------WQHEVTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIGAETNGYDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDELQWY-----VIDGVLTITAKPASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FANTSADQLHANQFSLALDRSVLTQTFSDDFNTLQLSDGTSGVWDPKYWWAPEKGATLTG
                                                            AMRKF FDARGNWKWTWDDEGDNNAMQVDY IRVY
                                                                                                                                                                                                           YENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYND
                                                                                                                                                                                                                                                                                       TDT----SGFHKYGVLWTEEEIVWYFDDAAIARADTPSDMHD-
                                                                                                                                                                                                                                                                                                                                                       SDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               GTWP--PELDVVEMHGQD--PNTVTATVHSNETGSQTS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                       MLVNLAIGGMAGPPTDGLM--GG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGMLTTYSSFAQTYGYFEMRADMPDDQGAWPAFWLLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 167; DB 1;
Pred. No. 1.4e-06;
8; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keller M.,
                                                                381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenylate cyclase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 158;
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DHET_ACEPO
                                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                                                                                                               InterPro; IPR002372; -. IRR002372; -. Pfam; PF01011; Bacterial_PQQ; 6.
PROSITE; PS00363; BACTERIAL_PQQ_1; 1.
PROSITE; PS00364; BACTERIAL_PQQ_2; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics in the European Bioinformatics in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D00635; BAA00528.1; PIR; S14270; S14270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>+</del> <del>+</del> <del>+</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tamaki T., Fukaya M., Takemura H., Tayama K., Okumura H., Kawamura Y., Nishiyama M., Horinouchi S., Beppu T.; "Cloning and sequencing of the gene cluster encoding two subunits of membrane-bound alcohol dehydrogenase from Acetobacter polyoxogenes."; Biochim. Biophys. Acta 1088:292-300(1991).

-i- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: METHANOL).

-i- CATALTYIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-NBI1028;
MEDLINE-91159482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last senence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ALCOHOL DEHYDROGENASE (ACCEPTOR) PRECURSOR (E
                                                                                                                                                                                                                                                                                            Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P22619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acetobacter polyoxogenes.
                                                             212
 259
                               98
                                                                                          48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: PQQ AND HEME. SUBUNIT: HETEROTETRAMER (DEHYDROGENASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: MEMBRANE-BOUND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REDUCED ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPACE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMALLER UNKNOWN SUBUNITS)
KAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYRSEGKGDNLFLG 318
                                                                                         GGGNSEFQLYTQDGANSFVR-----
                              GVLDVWAMYGACTNTDNNGC----
                                                             GNGGSEF----
                                                                                                                        78; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; alpha
                                                                                                                                                                                                 738 AA;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   2MTA
                                                                                                                                                                                                                ; PQQ; Heme; 1
35
6 738
6 750
0 650
3 653
4 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                            -GARGFVSAFDAETGKVDWRFFTVP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-2001402;
                                                                                                                                                                                                 80840
                                                                                                                                   5.0%;
                                                                                                                                                                                                 Œ,
                                                                                                                                                                                              Periplasmic; Membrane; Signal.

POTENTIAL.

ALCOHOL DEHYDROGENASE [ACCEPTOR].

HEME (COVALENT) (BY SIMILARITY).

HEME (COVALENT) (BY SIMILARITY).

IRON (HEME AVIAL LIGAND) (BY SIMILARITY).

IRON (HEME AVIAL LIGAND) (BY SIMILARITY).

MW; 1EZB6ED7BCD92AF6 CRC64;
                                                                                                                        37;
                                                                                                                     Score 112.5;
Pred. No. 0.07
37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Acetobacteraceae;
                                                                                          -DGKLFIKPTLLADNINPQTGAPFGTD-FMYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  738
                                                                                                                     ); DB 1;
).072;
les 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALCOHOL
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                                                            NPKNEPDAASDSVLMN 258
                                                                                                                                                   Length
                                                                                                                       Indels
                            -YRTGAAGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ME, AND TWO
DEHYDROGENASE
                                                                                                                        155;
                                                                                                                     Gaps
                                                                                          97
                              125
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RESULT 6

XYNA_R
AC P29126
DT 01-DEC
CR MMINION
OC RUMINO
RX MEDLIN
RX MEDLIN
RX MEDLIN
RY MOLL M
CC -!- FU
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                                                                                                                                                                                     EMBL; Z11127; CAA77476.1; -
PIR; S18043; S18043.
PIR; S20907; S20907.
HSSP; P48793; IXND.
InterPro; IPR001000; -.
InterPro; IPR001137; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XYNA_RUMFL
P29126;
01-DEC-1992 (
01-DEC-1992 (
15-JUL-1999 (
BIFUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang J.X., Flint H.J.;
Zhang J.X., Flint H.J.;
"A bifunctional xylanase encoded by the xynA gene of the rumen
"A bifunctional xylanase encoded by the xynA gene of the rumen
"A bifunctional xylanase encoded by the xynA gene of the rumen
"A bifunctional xylanase encoded by the xynA gene of the rumen
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"A bifunctional xylanase encoded by the xynA gene of the xylanase encoded by the xylanase enc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS

    - I - FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYLO-OLIGOSACCHARIDES

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: XYLAN DEGRADATION.
SIMILARITY: IN THE N-TERMINAL SECTION;
G (FAMILY 11 OF GLYCOSYL HUDROLASES).
SIMILARITY: IN THE C-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F (FAMILY 10 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND DOMAIN 2 MORE XYLOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKAGES IN XYLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APFDQNFHFILN - - - VAVGGTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSPEAKQAFVKDLK-------GWIVAWDPQKQAEAW--RVDHKGPWNGGILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE----WGKPWLPQYENDNPWAGGTNL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MG----STMHWGPGWDDNRYWLTSLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKTGEFI-----SGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGD 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPVGDWLWPAIWMLPEDWVYGGW----PRSGEIDIIETIGNRD--FKNTGGEFLGIQ-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIVALKPETGEYVWHFQETPMDQWDFTSDQQIMTLDLPINGETRHVIVHARKNGFFYIID 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGGHNFAAMAFSP----KTGLVYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----IPPAMSARVRTFQ-----KYSFTHGR-------
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(Rel. 24, Last sequence update)
(Rel. 38, Last annotation update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ins linked by an asparagine/glutamine-rich 6:1013-1023(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Clostridium group; Clostridiaceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO CELLULASE FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELLULASE FAMILY
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PRINTS; PR00134; ĞLHYDRLASE10. PRINTS; PR00911; GLHYDRLASE11. PROSITE; PS00591; GLYCOSYL_HYDROL_F10;

Pfam; PF00331; Glyco_hydro_10; Pfam; PF00457; Glyco_hydro_11;

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Matches
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Best Local
                                                                                                                                                                                                                                                       _BACLI
                                                                                                                                                                        01-AUG-1992 (Rel. 23, Cr
01-AUG-1992 (Rel. 23, La
01-NOV-1997 (Rel. 35, La
BETA-GLUÇANASE PRECURSOR
(1,3-1,4-BETA-D-GLUCAN 4
                                                                                                                                                                                               01-AUG-1992
01-AUG-1992
01-NOV-1997
                                                                                                                                                                                                                                GUB_BACLI
P27051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; SIGNAL CHAIN DOMAIN DOMAIN ACT_SITE ACT_SITE ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00776; PROSITE; PS00777; Xylan degradation;
                   Lloberas J., Perez-Pons J.A., Querol E.;

"Molecular cloning, expression and nucleotide sequence of the endo-beta-1,3-1,4-D-glucanase gene from Bacillus licheniformis. Predictive structural analyses of the encoded polypeptide.";

Eur. J. Biochem. 197:337-343(1991).
                                                                                                               Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1402;
                                                                                                                                                  Bacillus licheniformis
REVISIONS
                                                                               MEDLINE-91224124; PubMed-2026156;
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYYIVEGWGD----
                                                                                                                                                                                                                                                                                                     ONMUNDOONNAMIO
                                                                                                                                                                                                                                                                                                                 QKPWSNGDWYNDAMRKFFDARGNWK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATEPQYWSVRQTSGSANNQTNYM-KGTIDVTKHEDAWSAAGLDMSGTLYEVSLNIEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNINPQ-----TGAPFGTDFMYNGVLDV-----WA-----MYGACTNTDNNG
                                                                                                                                                                                                                                                                                                                                                NNDWNQ-WNNQNNNQQNAWNGWDNNNNWNQN
                                                                                                                                                                                                                                                                                                                                                                       FWEWGKPWLPQYEN-DNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPAL
                                                                                                                                                                                                                                                                                                                                                                                              WNQWNNQGQQQNNDWNWGQQNNDWNQWNNQG-----QQQNN------
                                                                                                                                                                                                                                                                                                                                                                                                                     NRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGE-----FLGIQKMGSTMHWGPGWDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -YRSNGSANY-----KSVSVTQGGSSDNG-----GQQQNNDWNQQNNNQQQNNDWNWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                       el. 23, Last sequence update)
el. 35, Last annotation update)
PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        884
111362
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954
622
954
122
223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
19
                                                                                                                           Bacillus/Clostridium us group; Bacillus.
                                                                                                                                                                                                                                                                                                    -WNNQNNWNNNQQQNNDWNQWNNQGQQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                           - QNNDWNNWGQQNNDWNQWNQGQQQNNDWNNWGQQNND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR 28, OR 29 (POTENTIAL).
BLEUNCTIONAL ENDO-1,4-BETA-XYLA
XYLANASE DOMAIN 1.
ASN/GLN/TRP-RICH (LINKER).
XYLANASE DOMAIN 2.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 112.5;
Pred. No. 0.09
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosidase;
                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .096;
                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                          WDDEGDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENDO-1,4-BETA-XYLANASE XYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multifunctional
                                                                                                                                       group;
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                                                                                                                                                                                                                                                                                                     453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                NOQQNNWDWNN
                                                                                                                                                                                                                                                                                                                                                                                              -DWNNWGQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -WPAIWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme;
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                                                                                                                                                                                                                                                                                                                                                  410
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                                                                    Query Match
Best Local S
Matches 60
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Š В Ş В Ş B S 밁 20 밁 Ş

밁

60; Similarity

Conservative

42;

Mismatches

88;

Indels

84;

Gaps

18;

4.9%; 21.9%;

Score 110; Pred. No. 0

0

.034; B

1:

Length

243;

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MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                         CHAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucanohydrolase at 1.8-A resolution.";
FEBS Lett. 374:221-224(1995)
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF 1.4-BETA-D-GLYCOSIDIC
-IN BETA-D-GLUCANS CONTAINING 1.3- AND 1.4-BONDS.
-I- MISCELLANEOUS: BETA-GLUCANASES OF BACILIUS HAVE A SUBSTR-SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-I- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Planas A., Juncosa M., Lloberas J., Querol E.; "Essential catalytic role of Glul34 in endo-beta-1,3-1,4-D-glucan glucanohydrolase from B. licheniformis as determined by site-directions."
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Hahn M., Pons J., Planas A., Querol E., Hein
"Crystal structure of Bacillus licheniformis
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Planas A., Juncosa M., Lloberas J.,
"Essential catalytic role of Glu134
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PIR; S15388; S15388.
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J. Biol. Chem. 269:14530-14535(1994).
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PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
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MEDLINE=94237863;
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Juncosa M., Pons J., Dot T., Querol E., Planas A.;
"Identification of active site carboxylic residues in Elicheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase
                                                                                                                                                                                                                                                                                                                          Hydrolase;
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MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
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McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
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01-JUN-1994 (Rel. 29, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
STALIDASE PRECURSOR (EC 3.2.1.18) (NET
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"Role of Vibrio cholerae
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STRAIN-CLASSICAL OGAWA 395 / ATCC 39541 /
MEDLINE-92112298; PubMed-1730470;
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                                           LT2
                                                                 of neuraminidase
                                                                                                        MEDLINE-92389334; PubMed-1518058; Taylor G.L., Vimr E.R., Garman E.
                                                                                                                                                                                                     Vimr E.R., Lawrisuk L., Galen J.E., Ka

"Cloning and expression of the Vibrio

nanH in Escherichia coll.";

J. Bacteriol. 170:1495-1504(1988).
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-44 FROM N.A., STRAIN-CLASSICAL OGAWA 395 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salzberg S.L.,
Fraser C.M.;
                                                                                       "Purification,
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                                                                                                                                                                                                                                                                                                  MEDLINE=88169467; PubMed=2832365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M83562; AAA27546.1; -. EMBL; AE004255; AAF94933.1; EMBL; M19268; AAA27547.1; -. PIR; A43866; A43866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structure 2:535-544(1994).
-i- FUNCTION: CLEAVES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crenells S., Garman E.F., Laver W.G., Vimr E.R., Taylor G.L.; "Crystal structure of Vibrio cholerae neuraminidase reveals dual lectin-like domains in addition to the catalytic domain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02012; BNR;
                         213
                                                      246
                                                                                  155
                                                                                                                                                                        143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I- COFACTOR: CALCIUM.
I- SUBUNIT: MONOMER (PROBABLE).
I- SUBCELLULAR LOCATION: SECRETED.
I- INDUCTION: MAY BE CONTROLLED BY SIALI GROWTH-PHASE-DEPENDENT MECHANISM.
I- SIMILARITY: BELONGS TO FAMILY 33 OF G.
I- SIMILARITY: CONTAINS 4 BNR REPEATS.
                                                                                                               190
                                                                                                                                            98
                                                                                                                                                                                               44 VTATGGGNSE---FQLYTQDGAN----SFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIALIDASES HAVE BEEN SUGGESTED TO BE PATHOGENIC FACTORS IN MICROBIAL INFECTIONS. NANH FACILITARIES CHOLERA TOXIN BINDING TO HOST INTESTINAL EPITHELIAL CELLS BY CONVERTING CELL SURFACI POLYSIALOGANGLIOSIDES TO GMI MONOGANGLIOSIDES.

CAPALYTIC ACTIVITY: HYDROLYSIS OF 2,3-, 2,6- AND 2,8-GLYCOSIDI LINKAGES JOINING TERMINAL NON-REDUCING. OR O-ACYLNEURAMINYL RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACYLATEI RESIDUES TO GALACTOSE, IN OLIGOSACCHARIDES, GLYCOPROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CLEAVES THE TERMINAL SIALIC ACID (N-ACETYL NEURAL ACID) FROM CARBOHYDRATE CHAINS IN GLYCOPROTEINS PROVIDING SIALIC ACID WHICH CAN BE USED AS CARBON AND ENERGY SOURCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOLIPIDS OR COLOMINIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration
                                                         ٧
                                                                                  VGDWLWPAIWMLPEDWVYGGWP--RSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWG
                                                                                                               MI--VWG--NGSSNTDGVAAYRDIKFEIQGDVIFRGPDRIPSIVASSVTPGVVTAFAEKR 245
                                                                                                                                         GVLDVWAMYGACTNTDNNGCYRT---GAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMP 154
                                                                                                                                                                        VLATGTAATEYHKFELVFLPGSNPSASFYFDGK-----
                         PGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLID--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VC1784;
                                                                                                                                                                                                                                              Similarity
-DTELNLTEQINVSDEFDFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002860;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycosidase;
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                                                                                                                                                                                                                                Conservative
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                                                       GGDPGALSNTNDII-TRTSRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal;
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BNR 2
BNR 3
BNR 4
                                                                                                                                                                                                                                            Score 109; DB Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                      PROTON DONOR (BY S:
S -> L (IN REF. 3);
FA85ED907FB20AF0
                                                                                                                                                                                                                                                                                                                                                                                                         SIALIDASE
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat;
                                                                                                                                                                                                                                                                                                                   DONOR (BY SIMILARITY)
(IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIALIC ACID AVAILABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium;
                                                                                                                                                                                                                               107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                                                                                          Length 781;
                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the
                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure.
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LL SURFACE
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 PRPIYDPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND
                                                         -WTI-
                                                                                                                                                                                                                             Gaps
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                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     ROEMET T., PATAVICINI G., PAYTON M.A., BUSSEY H.;
"Characterization of the yeast (1-->6)-beta-glucan bios components, Krefep and Sknlp, and genetic interactions b PKCI pathway and extracellular matrix assembly.";
J. Cell Biol. 127:567-579(1994).
-:- FUNCTION: INVOLVED IN THE SYNTHESIS OF (1->6)- AND CILUCAN POLYMERS OF THE YEAST CELL WALL IN VIVO. IT FOR FULL ACTIVITY OF BETA-GLUCAN SYNTHASE, PART OF A MULTIPROTEIN GLUCAN BETA-GLUCAN SYNTHASE, PART OF A MULTIPROTEIN GLUCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roemer T.D., Fortin N., Bussey H.; "DNA sequence analysis of a 10.4 kbp region on the chromosome XVI positions GPH1 and SGV1 adjacent identifies two novel tRNA genes."; Yeast 10:1527-1530(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane protein required for glucan synthesis in v synthase activity in vitro."; Proc. Natl. Acad. Sci. U.S.A. 88:11295-11299(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Last sequence update)
BETA-GLUCAN SYNTHESIS-ASSOCIATED PROTEIN KRE6
RESISTANCE PROTEIN 6).
KRE6 OR YPR1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
KRE6_YEAST
 Phosphorylation.
DOMAIN 1
                                                                    EMBL; M80657; AAA34726.1; EMBL; L33835; AAB59312.1;
                         Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROemer T., Bussey H.;
*Yeast beta-glucan synthesis: KRE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P32486;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE-95014745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95176711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92107936;
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                                                                                                                                                                                                                                                               A MODULATOR.
SUBCELLULAR LOCATION:
SUBCOMPARTIMENT.
                                                                                                                                                                                                                                   SIMILARITY: STRONG,
                                    A41624; A41624.
S0006363; KRE6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed-7871892;
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27,
36,
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 252
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                                                                                                                                                                                                                                                                             TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sis: KRE6 encodes a predicted for glucan synthesis in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KPWLPQ--YENDNPWAGGTNLAPFD-----QNFHFI
                                                                                                                                                                                                                                    SKN1.
                         Cell wall; Signal-anchor;
CYTOPLASMIC
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(POTENTIAL)
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KRE6,
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? IS REQUIRED
). IT MAY BE A
NN SYNTHASE OR
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Best Local
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CARBOHYD
"Two beta-glycanase genes are clustered in Bacillus polymyxa: molecular cloning, expression, and sequence analysis of genes encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase.";
J. Bacteriol. 173:7705-7710(1991).
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC L:
IN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
                                                                                                                                                                                                    GUB_PAEPO STANDARD; PRT; 238 AA.
P45797;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                               SEQUENCE FROM N.A. STRAIN=ATCC 842;
                                                                                                                                             Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                   MEDLINE=92041687; PubMed=1938968;
                                                                                                                              NCBI_TaxID=1406;
                                                                                                                                                                     Paenibacillus
                                                                                                                                                                                           (1,3-1,4-BETA-D-GLUCAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGISYLPGQKLSICTCDVEDHPNQGVGRGAPEIDVLE--GETDTK-----IGVGIASQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGALEISANLPNYGRVSGLWPGLWTMGNLGRPGYLASTQGVWPYSYESCDAGITPNQSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGRVVVHAKMP-VG--DWLWPAIWMLPE-----DWVYGGWPRS----
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                                                                                                                                                                                                                                                                                                                                                                                                                     -NVTWYEFGEYGGYFQKYAIEYLND-
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                                                                                                                                          polymyxa (Bacillus polymyxa).
micutes; Bacillus/Clostridium gr
hylococcus group; Paenibacillus
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19.0%;
                                                                                                                                                                                           4-GLUCANOHYDROLASE) (LICHENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDIWYMPDYDFIEVYNFTTTMNTYAGGPFQQAVSAVSTL
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Pred.
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No. 0.
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(POTENTIAL).
(POTENTIAL).
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Best Local
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15-DEC-1998 (Rel
15-DEC-1998 (Rel
15-JUL-1999 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSTTE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Glycosidase; SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X57094; CAA40379.1; -. HSSP; P23904; ICPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
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           ADH
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                                                     STRAIN-DES11 / Thurner C.A.K.;
                                                                                                                      Bacteria; Proteobacteria;
Gluconacetobacter.
                                                                                  SEQUENCE FROM N.A.
                                                                                                           NCBI_TaxID=33995;
                                                                                                                                                     Acetobacter europaeus
                                                                                                                                                                                ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000757; -.
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SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     THGRVVVHAKMFVGDWLWFAIWMLFEDWVYGGWFRSGEIDIIETIGNRDFKNTGGEFLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVFW-EPLSYFNSSTWQ---KADGYSNGQMFNCTWRANNVNFTNDGKLKLSLTSPANN--
                                                                                                                                                                                                                                                                                                                        KHTATTNIP----STPGKIMMNLWNGTGVDSWLGSYNGANP
                                                                                                                                                                                                                                                                                                                                                   ENQALLDVPYPLIDANPWWVDFWEWG----KPWLPQYENDNP 294
                                                                                                                                                                                                                                                                                                                                                                                                        QKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYG----DNFHTFWFDWSPNGLRFFVDD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long and this statement is not removed.
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129
133
56
238 AA;
                                                                                                                                                                             (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 38, Last annotation update)
YDROGENASE [ACCEPTOR] PRECURSOR (EC 1.1.99.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                 / DSM 6160;
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AND HEME (BY SIMILARITY)
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129
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                                                                                                                                      alpha subdivision;
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Pred. No. 0.
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BY SIMILARITY.
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NUCLEOPHILE (BY SIMILARITY).
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OSTA_HAEIN
ID OSTA_HAEIN
AC P44846;
DT 01-NOV-1995
DT 01-NOV-1995
DT 30-MAY-2000
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Best Local :
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BINDING
METAL
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01011; Bacterial_PQQ; 6.
PROSITE; PS00363; BACTERIAL_PQQ_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X82894; CAA58066.1;
EMBL; Y09480; CAA70688.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND TWO SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDROGEN COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPACE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNGGSEF-----GARGFVTAFDAETGKVDWRFFTAP----
                                                                                                                                                          ONFHFILN - - - VAVGGTNG
                                                                                                                                                                                       AKQAFVKDLK - - -
                                                                                                                                                                                                                   GLRFFYDDENQALLDVPYPLIDANPWWVDFWE---WGKPWLPQYENDNPWAGGTNLAPFD
                                                                                                                                                                                                                                              NFAAMAFSP----KTGLVYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIPDSPE
                                                                                                                                                                                                                                                                           --STMHWGPGWDDNRYWLTSLP-----
                                                                                                                                                                                                                                                                                                      IDAKTGEFISGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGDLGGH
                                                                                                                                                                                                                                                                                                                                                            LGSIVALKPETGEYVWHFQETPMDQWDFTSVQQIMTLDLPINGETRHVIVHAPKNGFFYI
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                                                                                                                                                                                                                                                                                                                                                                                                                      NKAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADL-VYLGVGNGSPWNYKYRSEGKGDNLF
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IPR001479;
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651
655
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                                                           STANDARD;
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  32,
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739 A
651 H
654 H
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  Created)
Last sequence user that annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106; DB Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEME (COVALENT) (BY SIMILARITY).
HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIM;
E681BB237ACB91F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

ALCOHOL DEHYDROGENASE [ACCEPTOR].
                                                             PRT;
                                                                                                                                                                                       -GWIVAWDPQKQAEAW--RVDHKGPWNGGILATGGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      influenzae Rd.";
Science 269:496-512(1995)
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MEDLINE=95350630; PubMed=7542800;
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Haemophilus influenzae.
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385 LDFNYHKYDLANGWLNFKLHSQAVR--FD
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                                                                                                                                                                                                                                                      --HGRVVVHA----
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                                                                                                           -- KRHLFYWNHNSSFLQNW
                                                                                                                                      SLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE-WG
                                                                                                                                                                   TFTPKYMSRRGWQANGEFRYLTSIGE--
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HI0730; -.
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83; Conserv
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llarity 21.3%;
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                                                     ARIAYYQPNYNFSLS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma
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ORGANIC SOLVENT TOLERANCE
HOMOLOG.
E73C8A5786B02D1B CRC64;
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411
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                                                                                                           RLNINYTRVSDKRYFNDFDSIYG
                                                                                                                                                                                                                                                    ----DWLW----PAIWML---
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RESULT 13

XYND_RUMFL
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DO 11-NOV
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Interpro; IPR00137; -.
Interpro; IPR00137; -.
Pfam; PF02018; CBD_6; 1.
Pfam; PF00457; Glyco_hydro_16; 1.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE11.
PROSITE; PR00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DOMAIN
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15-JUL-1999 (Rel. 38, Last annotation update)
XYLANASE/BETA-GLUCANASE PRECURSOR (INCLUDES: ENDO-1,4-BETA-XYLANASE
(EC 3.3.1.8) (XYLANASE); (ENDO-BETA-1,3-1,4 GLUCANASE) (EC 3.2.1.73)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE)].
                                                                                                                                                                                                                               CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S61204;
HSSP; P23904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucanase domains, flavefaciens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence up 15-JUL-1999 (Rel. 38, Last annotation
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01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flint H.J., Martin J., McPherson C.
"A bifunctional enzyme, with separa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-17
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                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1
                                                                                                                                                                                                                                                                                                    Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINKAGES IN XYLANS.

CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES IN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 175:2943-2951(1993).
FUNCTION: CONTAINS TWO CATALYTIC I
BETA-1,3-1,4 GLOCANASE ACTIVITIES
CATALYTIC ACTIVITY: ENDOHYDROLYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G (FAMILY 11 OF GLYCOSYL HYDROLASES). SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: XYLAN DEGRADATION. SIMILARITY: IN THE N-TERMINAL
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                                                                                                               LINKER.
C (BETA-GLUCANASE).
NUCLEOPHILE (BY SIMILARITY)
PROTON DONOR (BY SIMILARITY)
                                             NUCLEOPHILE (BY POLY-THR. POLY-THR.
                                                                                                                                                                                                                               XYLANASE/BETA-GLUCANASE A (XYLANASE).
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                                                                                                                                                                                                                                                                                                                            Glycosidase;
    2880A689647284AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECTION;
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                                                                                            SIMILARITY)
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Best Local
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P07980;
P07980;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
             Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                Hofemeister J., Kurtz A., Borriss R., Knowles J.;
"The beta-glucanase gene from Bacillus amyloliquefaciens shows
extensive homology with that of Bacillus subtilis.";
Gene 49:177-187(1986).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES
-!- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGI
SIMILAR TO LICHENASE OF GERMINATING BARLEY.
                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=1390;
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                            PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                          Pfam; PF00722; Glyco_hydro_16;
                                                                                                                                        EMBL; M15674; AAA87323.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus amyloliquefaciens.
                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                         A29091; A29091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVDDWLKAFNGRTPLTAHYQWVTYNKNGVQHSSQGQNPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKHEKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRATQDIPKTPGKIMMNAWPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKHSDDWNYG----DNFHTFWFDWSPNGLRFFVDDEN--QALLDVPYP---LIDANPW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYHYGYYECSMQAMKNDGVVSSFFTYTGPS-DDNPWDEIDIEILGKNTTQVQFNYYTNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYNGYLDVWAMYGACTNTDNN--GCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----WVDFWEWGKPWLPQY------ENDNPW
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                                                                                                            P27051;
                                                                                                                                                                       an email to license@isb-sib.ch).
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                                                                                          IPR000757;
                             Glycosidase; Signal.
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Pred. No. 0.
BETA-GLUCANASE
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                                                                                                                                                                                                                    There are no restrictions ng as its content is in
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Best Local
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRE6_CANAL
P87023;
01-NOV-1997
                                                                           entities
or send a
                                                                                                                                                                                                                                         "Isolation of the Candida albicans homologs of Saccharomyces cerevisiae KRE6 and SKN1: expression and physiological function.";
J. Bacteriol. 179:2363-2372(1997).
-:- FUNCTION: INVOLVED IN THE SYNTHESIS OF (1->6)- AND (1->3)-BETA-D-GLUCAN POLYMERS OF THE YEAST CELL WALL IN VIVO. IT IS REQUIRED FOR FULL ACTIVITY OF BETA-GLUCAN SYNTHASE IN VITRO. IT MAY BE A BETA-GLUCAN SYNTHASE, PART OF A MULTIPROTEIN GLUCAN SYNTHASE OR
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans
                                                                                                        modified
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                                                                                                                                                                                                                                                                                                                                                    Mio T.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRE6
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01-NOV-1997
                                                  EMBL; D88490; BAA19593.1;
                                                                                                                                                                                                                                                                                                                                        Yamada-Okabe H.;
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                                                                                                                                                                                      SUBCOMPARTIMENT.
SIMILARITY: STRONG, TO SKN1.
                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI
                                                                                                                                                                                                                               A MODULATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYEVRMKPAKNTGIVSSFFTYTGPTE--GTPWDEIDIEFLGKDTTKVQFNYYTNGAGNHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                           s requires a license agreement (See http://www.isb-sib
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                       Yamada-Okabe
                                                                                                     non-profit institutions as long as its content and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
57
239
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(Rel. 35, Last annotation update)
SYNTHESIS-ASSOCIATED PROTEIN KRE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 35, Created)
(Rel. 35, Last seq
(Rel. 35, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Yeast).
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abe T., Yabe T.,
                                                                                                                                                                                                                                                                                                                                                                                                                      mitosporic
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         Cell wall; Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 104.5; DE Pred. No. 0.094;
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BY SIMILARITY.
; A76A64268A7AAA0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycotina; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                       Arisawa
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                                                                                                      for commercial
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Glycoprotein;

Transmembrane;

MEMBRANE PROTEIN)

TRANSMEM

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4.6%; Score 103.5; DB 1; Length 740;
Best Local Similarity 17.1%; Pred. No. 0.4;
Matches 78; Conservative 48; Mismatches 126; Indels 203; Gaps
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SEQUENCE
657 -LILNLGISNNWAYIDWPSISEPVTFRIDYVRVYQ 690
                                                              627 --GDDP-----TLTVYSQALH------ 656
                                                                                         289 YENDNPWAGGTNLAPFDONFHFILMVAVGGTNGFIPDGCINRGGDPALOKPWSNGDWYND 348
                                                                                                                            594 VTWYEFGDNAHNF----QTYGYEYLNDPETGYL-----
                                                                                                                                                        229 SDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQ 288
                                                                                                                                                                                       534 SSGKKENCGVASQSLQLAPMDIWYIPDYNWVEIYNFSVSTMNTYTGGPFQQALSATTMLN 593
                                                                                                                                                                                                                                                      474 YSYDSCDAGITPNOSSPDGISYLPGORLNKCTCPGELHPNRGVGRGAPEIDVIEGEVMTD 533
                                                                                                                                                                                                                                                                                      177 RS-------GEIDIIE----- 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 DGSEWYLVFSDEFD------ 377
                                                                                                                                                                                                                        186 TIGNRDFKNTGGEFLGIQKMG------STMHWGPGWDDNRYWLTSLPKH 228
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                                                                                                                                                                                                                                                                                                                                                                                                             80 DNINPQTGAPFGTDFMYNGVLDV-WAMYGACTNT------DNNGCYRTGAAGDI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 DWDQYHIYWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLA 79 | : | : | : | |
                            AMRKFFDARGNWKW-TWDDEGDNNAMQVDYIRVYK 382
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740 AA;
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18 201
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82456 MW;
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POLY-GLY.

POLY-GLY.

POLY-SER.

N-LINKED (GLCNAC. . .) (POI

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POLY-GLU.
POLY-SER.
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Search completed: October 11, 2001, 15:57:06 Job time: 298 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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 703
390.5
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1: sp_archea:*
2: sp_bacteria:
3: sp_fung1:*
  100.0
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Gapop 10.0 , Gapext 0.5
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2240
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                                                                                                                                                                                                                                                                                                                                         sp_plant:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
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017492 anopheles g
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Q45095 bacillus ci
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1 bombyx mori
1 oerskovia x
2 hyphantria
2 drosophila
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0 flavobacter
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clostridium
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4.8	4.8	4.8	4.8	4.8	4.9	4.9	5.0	5.1	5.2	5.4	5.6	5. 6	5.9	6.2	6. 6	8.0	8.2	8 . 5	9.3	10.7	11.1	11.1	11.5	12.3	12.7	
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Q9p6t0 neurospora	084907 zobellia ga	Q06472 saccharomyc	013789 schizosacch	O80803 arabidopsis	074170 aspergillus	Q9rii9 aeromonas s	Q9m0d2 arabidopsis	P93670 hordeum vul	Q9ker4 bacillus ha		O31530 bacillus su			007242 mycobacteri	Q84415 paramecium		Q9kwf3 clostridium				Q9nha9 drosophila	Q9vvr4 drosophila	073951 pyrococcus		Q9wxn1 thermotoga	

ALIGNMENTS

Qу	Qy Db	Оу	Qu Be	RESULT O77072 ACC ODT ODT OS OS CC OCC OCC OCC OCC OCC OCC OCC OC
121 GAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGE 180 	61 GANSEYRDGKLEIKPTLLADNINPOTGAPEGTDEMYNGVLDVWAMYGACTNTDNNGCYRT 120 	1 MRWTLYVLCLLFGEGFAFTDWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQD 60 	Query Match 100.0%; Score 2240; DB 5; Length 384; Best Local Similarity 100.0%; Pred. No. 1e-182; Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps	ILT 1 772. PRELIMINARY; PRT; 384 AA. 077072; 071072 PRELIMINARY; PRT; 384 AA. 077072; 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1998 (TREMBLRel. 08, Last sequence update) COELONIC CYTOLYTIC FACTOR 1. CCF1. Elsenia foetida (Common brandling worm) (Common dung-worm). Elwaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida; Lumbricina; Lumbricidae; Eisenia. NCBI_TAXID-6396; 1] SEQUENCE FROM N.A. MEDLINE-98406152; PubMed-9733802; Beschin A., Bilej M., Hanssens F., Raymakers J., Van Dyck E., Revets H., Brys L., Gomez J., De Beatselier P., Timmermans M.; "Identification and cloning of a glucan- and ilpopolysaccharide- binding protein from Eisenia foetida earthworm involved in the activation of prophenoloxidase cascade."; J. Biol. Chem. 273:24948-24954 (1998). EMBL; AF030028; AAC35887.1; EMBL; AF030028; AAC35887.1;

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Matches 148
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Lee S., Wang R., Soderhall K.;
"A lipopolysaccharide- and beta-1,3-glucan-binding in the photosomer of the freshwater crayfish Pacifastacus Legurification, characterization, and cDNA cloning.";
J. Biol. Chem. 275:1337-1343(2000).
EMBL; AJ250128; CAB65353.1; -.
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01-MAY-2000 (TEEMBLrel. 13, Last sequence update)
01-MAY-2000 (TEEMBLrel. 13, Last annotation update)
LIPOPOLYSACCHARIDE AND BETA-1,3-GLUCAN BINDING PROT
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                                                                                                                                   GRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQK 204
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                                       PYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIP
                                                                                                                     GRVEVRAKMPRGDWLWPAIWLMPKDSRYGGWPASGEIDIVESRGNNDYGN-----
                                                                                                                                                                     TSKWYSEHFLFNDELN----LGDKCTDHRDYGCVRKGTSEHIINPIMSAKFTTHPSFAFRY
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DGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWD-DEG---DNNAMQVDYIRV
                                                                      AGSTLHWGPNPQANMFLKTHKTYSANDGSFANNFHIWRMDWTRDNMKFYVDDQLQLTVDP
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K MEDLINE-96270625; PubMed-8692900;

K MEDLINE-96270625; PubMed-8692900;

T Molecular cloning of the first metazoan beta-1,3 glive of the sea urchin Stronglocentrotus purpuratus.";

T of the sea urchin Stronglocentrotus purpuratus.";

T of the sea urchin Stronglocentrotus purpuratus.";

T proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).

RIL Proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).

DR EMBL; U49711; AAC47235.1; -.

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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
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BACTERIA BINDING PROTEIN PRE
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                                                                                                                                                                                         01-OCT-2000 (Tremblrel. 15, 01-OCT-2000 (Tremblrel. 15, 01-OCT-2000 (Tremblrel. 15, BETA-1,3-GLUCAN RECOGNITION
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Molecular immune responses of the mosquito Anophel
bacteria and malaria parasites ";
Proc. Natl. Acad. Sci. U.S.A. 94:11508-11513(1997).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culi
   Eukaryota; Metazoa; Arthropoda; Tracheata; Pterygota; Neoptera; Endopterygota; Lepidop Bombycoidea; Bombycidae; Bombyx. NCBI_TaxID=7091;
                                                                                                                                                      Bombyx mori (Silk moth).
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Pred. No. 5.
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SEQUENCE FROM N.A.
STRAIN-KINSHU X SHOWA;
MEDLINE-20138243; PubM
Ochiai M., Ashida M.;
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SEQUENCE
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SIGNAL
MEDLINE-94033858; pubMed=7764221; Yamamoto M., Aono R., Horikoshi K.; Yamamoto M., Aono R., Horikoshi K.; Paricture of the 87-kDa beta-1, 3-glucanase gene IAMI165 and properties of the enzyme accumulated Escherichia coli carrying the gene."; Biosci. Biotechnol. Biochem. 57:1518-1525(1993). EMBL; D17519; BA044650.1; -.
                                                                                                                                                                                                                                       Bacillus circulans.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=1397;
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EMBL; AB026441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SALQVDYVKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSIGLNVAGIREFSED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGD
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hem. 275:4995-5002(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SKKLYAGPIMTGSDPYRSFYLKENIGYESWN---NDFHNYTLEWRPDGITLLVDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493
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16,
                                                                                                                                                                                                                                                                group;
                                                                                                                                                                                                                                                                                                                                                        PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                          Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 390.5;
Pred. No. 3e-2
i7; Mismatches
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BETA-1,3-GLUCAN RECOGNITION
9249039F7456BF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ISNKPWKNS--ATKAMLKFWDARSQWFPTWDED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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No. 3e
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                                                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                          Bacillus circulans
the periplasm of
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SEQUENCE
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Babril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01034; GI SMART; SM00409; IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000757; -.
InterPro; IPR003343; -.
InterPro; IPR003599; -.
Pfam; PF02368; Big_2; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera; Musc Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                            Q9VVR5
                                                                                                                                                                                                                                                                                       GNBP1 OR CG6895.
                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=BERKELEY;
                                                                                                                                                  MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                              CBI_TaxID=7227;
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1-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFHFILNVAVGGT--NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGEFLGIQKMGSTMHWGPGWDDNRYWLISLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TMQVDYVRVYK 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFYLIMNLAIGGTFDGGRTPD----PSDIPA----
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                                                                                                                                                                                                                                                                                                               Created)
Last sequence up
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Pred. No. 3.
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C4D2CFF93019446C
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                                                                                                                                                                                                                                                                                                                                                                            492
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3.7e-23;
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                                                                                                                                                                                                                                          Brachycera; Muscomorpha;
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McNount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang R.H., Wang X.,
RA Williams S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Williams S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Williams S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RT Typases, Franchold T., Rubin G.M., Venter J.C.;
RT Science 287:2185-2195(2000).
DR EMBL, AE003519, AAF49244.1;
-. DR EMBL, AE003519, AAF49244.1;
-. DR
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Q59328;
Q59328;
01-NOV-1996
01-NOV-1996
01-MAR-2001
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Hostin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFAFQYGRIEIRAKLPKGDWIVPLLLLEPLTEWYGQSGYESGQLRVALARGNSVLRMPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYSFTHGRVVVHAKMPVGDWLWPAIWMLP-EDWVYGGWPRSGEIDIIETIGNRDFKNTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTGAPFGTDFMYNGVLDVWAMYGACTNTDN--NGCY----RTGAAGDIPPAMSARVRTFQ 138
                                                                                                                                                                                 -ALKIDYVRVF
                                                                                                                                                                                                                      NAMOVDYIRVY
                                                                                                                                                                                                                                                              SLGVSVGGFGDF-----VDHLRTATYEKPWAN--YHPQAKLQFHQAQDQWLPTWKQP---
                                                                                                                                                                                                                                                                                                     ILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                              LFSVDGQVYGEMLNGFTELDENP---
                                                                                                                                                                                                                                                                                                                                                                                 REFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHF
                                                                                                                                                                                                                                                                                                                                                                                                                         KLVD----GRSLYGGP-----VLSTDAHQREDLWLSKRKISHFGDDFHTYSLDWSSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDW-----NYGDNFHTFWFDWSPNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLS-----IANSRLD---LSERCTGTHNRIKECILHSTGSGPSGIMPPIVTPRISTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLFEETFDQLNESLWIHDVRLPLDSKDAEFVLY--DG-KAKVHDGNLVIEP-LLWSSYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101;
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                      381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.9%;
  16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 357; 
pred. No. 2.1e-22;
pred. t-ches 133;
Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C5D0E5E61FABB779 CRC64;
                                                                                  1324
                                                                                ₿
                                                                                                                                                                                                                                                                                                                                              RWKQGGPMAPFDKMFYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Lai Z.,
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RESULT
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Best Local Similarity 27.2
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InterPro; IPR003305; ...
Pfam; PF00395; SLH; 3.
Pfam; PF02018; CBD_6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schwarz W.H., Schimming S., Fuchs K.P., Staudenbauer W.L.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: EMDOHYDROLYSIS OF 1,3- OR 1,4-ILINKAGES IN
BETA-D-GLUCANS WHEN THE GLUCOSE RESIDUE WHOSE REDUCING GROUP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridium.
                   Rhodothermus marinus.
Bacteria; CFB group;
NCBI_TaxID=29549;
                                                                              01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-CCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-DSM 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium thermocellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENDO-1,3(4)-BETA-GLUCANASE
(ENDO-1,3-BETA-GLUCANASE) (
                                                                                                                     052754;
                                                                                                                                052754
SEQUENCE FROM N.A.
                                                                       AMINARINASE.
                                                                                                                                                                                           999
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                                                                                                                                                                                                                                         645
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                                                                                                                                                                                          YVRVYQKD
                                                                                                                                                                                                                                                                                                                                                                                               YSFTHGRVVVHAKMPVGDWLWPAIWMLPEDW-VYGGWPRSGEIDIIETIGNRDFKNTGGE
                                                                                                                                                                                                                 YIRVYKRN
                                                                                                                                                                                                                                                              GGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVD
                                                                                                                                                                                                                                                                                                              QALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGG--TNLAPFDQNFHFILNVAV
                                                                                                                                                                                                                                                                                                                                                           FLG TOKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KEDITEPSGETYHYT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQYHIVWQDEFD--YFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKFTLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVOLVED IN THE LINKAGE
                                                                                                                                                                                                                                                                                                                                    ----DKIYGTIHFGEPHKESQGTYT-LP---EGQTFADDFHVYSIEWEPGEIRWYIDGK-
                                                                                                                                                                                                                                                                                                                                                                                     KSWKYGKFEIRAKMPQGQGIWPAIWMMPEDEPFYGTWPKCGEIDIMELLGHEP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEWRLVWSDEFNGSEINMANWSYDDPTNGRWNGEVQSYTQN--NAYIKDGALVIEAR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X89732; CAA61884.1;
P14090; lULO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1324 AA;
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                           673
                                                                                                                                                                                                                 384
                                                                                                                                                                                                                                         GGWPG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%;
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                                 Rhodothermus
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                                                                                 15,
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                                                                               Last sequence update)
                                                                                                        Created)
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Pred. No. 1.6e-21;
1; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            038E40F9E09538AB CRC64;
                                                                                                                                                                                                                                         ·YPDETTVF
                                  group;
                                                                                                                                                                                                                                                                                      YSRD-PYLADDYTYPAPFDQNFFLILNISV
                                                                                                                                276
                                  Rhodothermus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group;
                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1324;
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                                                                                                                                                                                                                                        -PQQMVVD
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Best Local
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                                                                                                                                                                                                                                                    O68641;
O68641;
O1-AUG-1998 (TrEMBLrel. (
O1-AUG-1998 (TrEMBLrel. (
O1-MAR-2001 (TrEMBLrel. )
                                           Parrado J., Escuredo P.R., Coneje
Asenjo J.A., Dobson C.M.;
"Molecular characterisation of a
                                                                                                                     Enzyme
[2]
                                                                                                                                                                                   Oerskovia xanthineolytica.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Cellulomonadaceae; Cel
NCBI_TaxID=1826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOTTISS R., KIAH M.;

BOTTISS R., KIAH M.;

SUBMILTED (FEB-1998) to the EMBL/GenBank/DDBJ database:

EMBL; AF047003; AAC69707.1; -.

InterPro; IPR000757; -.

Pfam; PF00722; Glyco_hydro_16; 1.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; I.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; I.
                                                                                  SEQUENCE FROM N.A.
STRAIN=LL G109;
MEDLINE=96409238; PubMed=8814220;
                                                                                                                                                                                                                                          BETA-1,3-GLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ITI278;
STRAIN-LL G109;
         SEQUENCE FROM N.A.
                                Biochim.
                                          Derskovia xanthineolytica.
                                                                                                                                         Ventom
                                                                                                                                                     STRAIN=LL
                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTDNNGCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDW
                                                                                                                                                                                                                                                                                                                                                                        LQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRVYK
                                                                                                                                                                                                                                                                                                                                                                                                            VYGG--WPRSGEIDIIETIG-NRD-----FKNTGGEFLGIQKMGSTMHWGPGWDDNRYW
                                                                                                                                                                                                                                                                                                                                                        -----LVVDYVRVYR
                                                                                                                                                                                                                                                                                                                                                                                                  ADWRHW
                                                                                                                                                                                                                                                                                                                                                                                                                                             -IRVPTARTD-----FHVYAIEWTPEEIRWFVDDSLYYRFPNERL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYGSAYWPDNGEIDIMEHVGFNPDVVHGTVHTKAYNHLLGTQRGGS---
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                                                                                                                              A.M., As
Microb.
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                                Biophys.
                                                                                                                                                   G109;
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                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                               Asenjo J.A.;
b. Technol. 13:71-75(1991).
                                Acta
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16,
                                                                         Conejero-Lara F.,
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Last sequence update)
Last annotation update)
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                                                      thermoactive
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                                                                          Kotik M.,
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                                                      beta-1,3-glucanase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                 Cellulomonas.
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                                                                         Ponting
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                                                                          C.P.,
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RESULT Q9NJ98
ID Q9
AC Q9
AC Q9
AC Q9
CO Q9
CO Q9
CO Q9
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Q9NJ98;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 15, Last annotation update)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
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Pfam; PF00652; Ricin_B_lectin; 1.
Pfam; PF0722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
SMART; SM00458; RICIN; 1.
TISSUE=FAT BODY;
MEDLINE=20179841; PubMed=10713054,
Ma C., Kanost M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96250169; PubMed-8659924; Ferrer P., Hedegaard L., Halkier T., Diers I., Savva D., Asenjo J "Molecular cloning of a lytic beta-1,3-glucanase gene from Oerskc xanthineolytica LLG109. A beta-1,3-glucanase able to selectively permeabilize the yeast cell wall."; hnn. N. Y. Acad. Sci. 782:555-566(1996).
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HSSP; P23904; 1AJK.
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI_TaxID=7130;
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                                                                                                                                                                                Kim Y.S., Ryu J.H., Han S.J., Choi K.H., Brey "Molecular cloning and functional analysis of Gram-negative bacteria binding protein family
                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                          GRAM-NEGATIVE BIGNBP1 OR CG6895
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                                                                                                                           SEQUENCE
                                                                                                                                                    Submitted (JAN-2000) to the EMBL/GenBank/DDBJ EMBL; AF228472; AAF33849.1; -.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
Kim Y.S., Ryu J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A betal,3-Glucan Recognition Protein from an Insect, Manduca sexta,
Agglutinates Microorganisms and Activates the Phenoloxidase Cascade.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKYGRVEISAKMPRGDWLVPLIQLEPVNKNYG--IRNYVSGLLRVACVKGNTEYIKTLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPR---SGEIDIIETIGNRDFKNT--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TAFGEDAIWK-TLD---LSDRCTGLLGTAQCKRDPSDAIIVPPIVTAKINTKKTFA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNG-CYRTGA-AGDIPPAŃSARVRTFQKYS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLFEDNFNKPLADGRIWTPEIMFPGEPDYPFNVYMKETDNLHVGNGNLVIKPMPLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GIVYGRVTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNP-----WAGGTNLAPFDQNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 14.7%; al Similarity 28.4%; 106; Conservative !
                                                                 Similarity
                                                                                                                          FBgn0040323;
494 AA; 55
                                                                                                                                                                                                                                                                                                                                     (TIEMBLIE1. 15, Created)
(TIEMBLIE1. 15, Last sequence update)
(TIEMBLIE1. 16, Last annotation update)
E BACTERIA BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485
                                                                                                                           55455
                                                                 14.48; 26.28;
                                                                                                                                         GNBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EAEPYRTANLKEFISNEPWINEFHNYTLEWSPDAITMAVD-
                                                                                                                           ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 329.5;
Pred. No. 4.5e
55; Mismatches
                                                     Score 323; DB 9
Pred. No. 1.6e-1
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3BA4869C5ADE934A CRC64,
                                                                                                                           461DF8E363EA312B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- KPWKN--TATKAMVNFWNARSQWNPTWLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PAGGEYKEANEQNVEAAARWIQGSNIAPFDDMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 4.5e-20;
smatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                             494
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                                                                                                                                                                                                                                                                                               Hexapoda;
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                                                                                   Ģ
                                                                                                                                                                                                                                                                                  Brachycera;
                                                                                                                                                                                                             P.T.,
                                                                                                                                                                      databases
                                                                                                                                                                                    Drosophila
.";
                                                                                                                           CRC64;
                                                                              Length
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                                                                                                                                                                                                               W.J
                                                                                                                                                                                                                                                                                  Muscomorpha;
                                                                                                                                                                                              melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77;
                                                       76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cascade.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                     Gaps
227
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Best Local s
Matches 101
                                                                                                                          CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-MAY-2000 (TREMBLREL. 13, Last annotation update)
GRAM-NEGATIVE-BINDING PROTEIN PRECURSOR (GNBP).
                                                                                                                                                                                  Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                         bacteria-binding protein from the silkworm, Bombyx mori.";
Proc. Natl. Acad. Sci. U.S.A. 93:7888-7893(1996).
-i- FUNCTION: MAY BE INVOLVED IN THE INSECT-IMMUNE PROTEIN. IT
STRONG AFFINITY TO THE CELL WALL OF GRAM-NEGATIVE BACTERIA.
-i- SUBCELLULAR LOCATION: SECRETED IN HEMOLYMPH.
-i- TISSUE SPECIFICITY: FAT BODY AND TO A LESSER DEGREE IN
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE TISSUE-FAT BODY, AND HEMOLYMPH; MEDLINE-96353914; PubMed-8755572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bombyx mori (Silk moth),
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexap
Pterygota; Neoptera; Endopterygota; Lepidoptera;
Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-7091;
                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                              Lee W.J., Lee J.D., Kravchenko V.V., Ulevitch R.J., Brey P.T.;
Purification and molecular cloning of an inducible gram-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430
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 147
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                           27
                                                                                                                                                                                                                                                                   CUTICULAR EPIDERMAL CELLS.
DEVELOPMENTAL STAGE: EXPRESSION
OR MICROBIAL CHALLENGE.
                                                                                                                                                                                                                           SIMILARITY: TO H.CUNEA GRAM-NEGATIVE-BINDING PROTEIN. SIMILARITY: WEAK, TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                       INDUCTION: BY BACTERIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDNNAMQVDYIRVY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDW-----NYGDNFHTFWFDWSPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKYSFTHGRVVVHAKMPVGDWLWPAIWMLP-EDWVYGGWPRSGEIDIIETIGNRDFKNTG
                           VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISLGVSVGGFGDF-----VDHLRTATYEKPWAT----IIPRRSCSSTRAQDQWLPTWKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKW--TWDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLFSVDGQVYGEMLNGFTELDENP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKLVD----GRSLYGGP-----VLSTDAHQREDLWLSKRKISHFGDDFHTYSLDWSSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETFAFQYGRIEIRAKLPKGDWIVPLLLLEPLTEWYGQSGYESGQLRVALARGNSVLRMPR
                                                                                                                                                                                         IMILARITY: warn,
L38591; AAB40946.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTGAPFGTDF-MYNGVLDVWAMYGACTNTDN--NGCY----RTGAAGDIPPAMSARVRTF
IFEEQFDSLDENVWQIEQYIPIYHPEYPFVSYQRNNLTVSTADGNLHI--
                                                       101;
                                                      Similarity 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ALKIDYVRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -YRRDLSIANSRLD---LSERCTGTHNRIKECILHSTGSGPSGIMPPIVTPRISTK
                                                                                                                        119
182
467
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52217
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467
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                                                                   14.0%;
                                                                                                                             WW.
                                                       58;
                                                      Score 314; DB pred. No. 8.9e 8; Mismatches
                                                                                                                          GRAM-NEGATIVE-BINDING PROTEIN,
N-LINKED (GLCNAC. . . ) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL)
; 780652FC89046B77 CRC64;
                                                                                                                                                                                               immunity
                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ဝှု
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                                                                     DB 5;
.9e-19;
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                                                                                                                                                                                                                                                                                   σ
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                                                                                                                                                                                                                                                                                   HOURS
                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glossata; Ditrysia;
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                                                       Indels
                                                                                                                                                                                                                                                                                   AFTER AN
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                                                       68
NAKLO
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                                                       Gaps
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01-NOV-1996 (TrEMBL)
01-NOV-1996 (TrEMBL)
01-MAY-2000 (TrEMBL)
BETA-1,3-GLUCANASE 1
                                                                                                                                                                                                                                                      Pfam; PFo
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q51333
                                                                                                                                                                                                                                                                                                                                                       Ferrer P., Halkier T., Hedegaard L., Savva D., Diers I., Asenjo "Nucleotide sequence of a beta-1,3-glucanase isoenzyme IIA gene Oerskovia xanthineolytica LL G109 (Cellulomonas cellulans) and i
                                                                                                                                                                                                                                                                                           EMBL; U56935; HSSP; P23904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BGLIIA.
                                                                                                                                                                                                                                                                                                                                subtilis.";
                                                                                                                                                                                                                                                                                                                                           characterization of the recombinant
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96345651; PubMed=8755914;
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-LL
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales;
NCBI_TaxID=1826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371
                         143
                                                  141
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 GIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT
                         QPQFGRIEARIQIPRGQGIWSAFWMVGANLPDTPWPTSGEIDIMENVGNAPHEVHG----
                                                  SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
                                                                                                                            LAWSDEFDGAAGSAPNPDVWNHETGAGGWGNAELQNYTTSRVNSAL-DGQ-
                                                                                                                                                  IVWQDEFDYFDGAK-----WQHEVTATGGGNSEFQLYTQDGANSFYRDGKLFIKPTLLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SLIVDFVKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGEFLGIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGTVEIRAKLPQGDWLYPEILLEPFLKKYGSMNYASGVVKIACARGNAELYSGPNDYSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN-----RDFKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QHMPGFLDDSIYSGTLN---LFSGCTSS-AEACIKQASGADILPPIVSGRI-TSIGFAFT
                                                                                                 NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY
                                                                                                                                                                                                                                        PF00722; Glyco_hydro_16; 1.
TE; PS01034; GLYCOSYL_HYDROL_F16;
NCE 306 AA; 32835 MW; CD8DB8C
                                                                                                                                                                             . Similarity
95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                         xanthineolytica.
Firmicutes; Actinobacteria; Actinobacteridae;
etales; Micrococcineae; Cellulomonadaceae; Cel
                                                                                                                                                                                                                                                                             IPR000757; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VLYGGPIMDLECRENFLSTKRRRDGTSWGDSFHTYSVQWTPDFIALSV
                                                                                                                                                                                                                                                                                                      178:4751-4757(1996)
AAC44371.1; -.
                                                                                                                                                                                                                                                                                            1AJK
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                                                                        GNLVITAL -----QESDGSY -----TSARLTTQGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01,
                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                           Score 307; DB 2;
Pred. No. 2.1e-18;
6; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                          CD8DB8C1A6F8DC04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAVCAHAPRHLLQAGSQMAPFDDHFYITLGV
                                                                                                                                                                                                                                                                                                                                             enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDSARKASVHFWRHMSDWFPRWSQP---
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                                                                                                                                                                                                   Length 306;
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cellulomonas
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                                                                                                                                                                                                                                                                                                                                              Bacillus
                                                                                                                                                                                                                                                                                                                                                                       Asenjo J.A.;
[A gene of
                                                                                                                                                                              134;
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           NON_TER
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              *ISOlation and characterization of immune-related genes from the fall webworm, Hyphantria cunea, using PCR-based differential display and subtractive cloning.";
Insect Biochem, Mol. Biol. 28:827-837(1998).
-!- FUNCTION: MAY BE INVOLVED IN THE INSECT-IMMUNE PROTEIN. IT PRESENT STRONG AFFINITY TO THE CELL WALLOF GRAM-NEGATIVE BACTERIA.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- DEVELOPMENTAL STAGES: EXPRESSION STARTS A FEW MINUTES AFTER AN INUTRY OR MICROBIAL CHALLENGE THEN STAYS RELATIVELY HIGH FOR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             096363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-99035790; PubMed-9818384;

Shin S.W., Park S.-S., Park D.-S., Kim M.G., Kim S.C., Brey P.T.,

Park H.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TERMBLIEL. 10, Created)
01-MAY-1999 (TERMBLIEL. 10, Last sequence update)
01-MAY-2000 (TERMBLIEL. 13, Last annotation.update)
GRAM-NEGATIVE-BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           096363;
                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: TO H.CUNEA GRAM-NEGATIVE-BINDING PROTEIN.
-i- SIMILARITY: WEAK, TO FAMILY 16 OF GLYCOSYL HYDROLASES EMBL; AF023916; AAD09290.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Noctuoldea; Arctiidae; Hyphantria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNBP1.
                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Insect immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=39466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hyphantria cunea (Fall webworm).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380
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                                                                                                                                                                      155
                 193
                                                                                                         209
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                                                                                                                                                                                                                                                                                                                                                                                                                   OR 24 HOURS. INDUCTION: BY BACTERIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VY 381
                                                              SETHGRVVVHAKMFVGDWLWFAIWMLFEDWVYGGWP-RSGEIDIIETIGNR------DF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGT
                                                                                                        --QQRMPGFTDSSIYSGSLNI---FSGCT-APAEACMKDAWGASILPPVVSGRI-TSKAF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TVH-GPGYSGDN--GIMGTYQHPQGWSEADDFHTFGIDWTPGEITWLVD--GQ
KNT---GGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNG 249
                                              NPQTGAPFGTD-FMYNGVLDVWAMYGACTNTDNNGCYRTG-AAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                      IFEENFNTFREDVWQIEQYIPVYSTEFPFVSYQHLSQDPTVA-VTGGNLRITPKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYHRVTTADVGANQW-----
                                                                                                                                                                                                                                 107;
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481 AA;
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                                                                                                                                                                                                                                                                                                           110
53014 MW;
                                                                                                                                                                                                                                              13.5%;
                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                Score 302; DB 5; 1
Pred. No. 9.7e-18;
1; Mismatches 146;
                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL); 49B2AC8C406929F6 CRC64;
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                                                                                                                                                                                                                                                           Length 481;
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                                                                                                                                                                                               322 SNKMLFGGPVMNLQ-CYDTLLESKASSNGRQW------GDDFHEYVLRWAPER 367
P----QLLVDYVKV 478
                              EGDNNAMQVDYIRV
                                                                                              NFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDD 366
                                                                                                                                                              LRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNP---WAGGTNLAPFDQ 306
                                                               HFYLTLGVAAGSITEF-PDGVQTSGSRP---KPWTNTG--SKAMLHFWEDMDSWFATWNQ 468
                                                                                                                                ITLSVDGVEWARVEPTASGLSGR-
                              380
                                                                                                                                ----FPQTCSKLPRTFLAAGTKMAPFDD
                                                                                                                                414
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Search completed: October 11, 2001, 15:56:45 Job time: 303 sec